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March 29, 2006, 01:38:52 ; Search time 124.25 Seconds (without alignments) 49.507 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Abo73099 Pseudomon	Abo83630 Pseudomon	Adx97192 Plant ful			Adg48250 Human ret	4	80		0 Peptide	Heparin	Aab71428 Peptide B	Abp00279 Human ORF					Aau62059 Propionib			Abo83790 Pseudomon	Abo68429 Pseudomon	Aau86821 Novel hum	Adb60155 Connectiv
SUMMARIES		QI	ABO73099	AB083630	ADX97192	ABO74539	ADH48840	ADG48250	AAU33234	ABP76678	AAB71432	AAB71430	AAY87840	AAB71428	ABP00279	ADX75905	AAU41918	ABM3 8437	ABP00666	AAU62059	ABM58578	ABP05425	AB083790	AB068429	AAU86821	ADB60155
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Abo72505 Pseudomon Adx87688 Plant ful Abo78160 Pseudomon	Abo75935 Pseudomon Adx78723 Plant ful Abo74930 Pseudomon abo82700 Pseudomon		Abo76573 Pseudomon Adx93670 Plant ful Abo73028 Pseudomon		Abm44121 Propionib Abo68472 Pseudomon Abo83595 Pseudomon Aag90194 C glutami Ady11827 Plant ful
ABO72505 ADX87688 ABO78160	ABO75935 ADX78723 ABO74930	ABU11486 AAU42224 ABM38743	ABO76573 ADX93670 ABO73028	ABO68892 ABO72617 AAU47602	ABM44121 ABO68472 ABO83595 AAG90194 ADY11827
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ALIGNMENTS

ABO73099 standard; protein; 133 AA.

The invention relates to Pseudomonas aeruginosa polypeptides and the polymuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa derived peptides for antibacterial drugs, production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection. Bacterial infection; Pseudomonas aeruginosa infection; antibacterial. Bush D; Disclosure; SEQ ID NO 21845; 455pp; English. Rubenfield MJ, Nolling J, Deloughery C, Pseudomonas aeruginosa polypeptide #5274. (GENO-) GENOME THERAPEUTICS CORP. 98US-0074788P. 98US-0094190P. 99US-00252991. (first entry) Pseudomonas aeruginosa. WPI; 2003-615309/58. N-PSDB; ABD06670. 18-FEB-1999; US6551795-B1 18-FEB-1998; 27-JUL-1998; 29-JUL-2004 22-APR-2003 ABO73099;

Pred. No. 2e+03;

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and the polymucleotides encoding them. The sequences are useful in diagnosis and the pathological conditions, as molecular tragets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of including anti-P. aeruginosa cargets for antibacterial drugs, including anti-P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
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of Pseudomonas species using blochip technology. Sequences AB067826-
Bob64396 represent P. aeruginosa polypeptides of the invention. Note: The
sequence data for this patent did not form part of the printed
specification but was obtained in electronic format from USPTO at
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                                                                                                                                                                                                                                                                   Score 19; DB 7; Length 133; Pred. No. 1.5e+03; 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nolling J, Deloughery C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO83630 standard; protein; 189 AA.
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                                                                                                                                        segdata.uspto.gov/seguence.html
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                                                                                                                                                                                                                                                                          33.3%;
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N-PSDB; ABD17201.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                           Sequence 133 AA;
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95.0%; Score 19; DB 7; Length 189;

Query Match

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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme smooth of the part and pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one carbes are sent or increased oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                    Gaps
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                    Indels
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8
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                  0; Mismatches
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                                                                                                                                                                              ADX97192 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2003; 2003US-00425114.
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05-NOV-2001; 2001US-00985678.
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                  4; Conservative
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Similarity
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ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein content
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Best Local &
Matches 4
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(CAOY/)
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                                                                                                                                         RESULT 3
                                                                                                                                                              ADX97192
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NOV53 protein sequence, SEQ ID 124.
                                                              ADH48840 standard; protein; 533 AA
                                                                                                          25-MAR-2004 (first entry)
     307 RRAASRSSRTAR 318
                                                                                     ADH48840;
                                                                                     The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a capterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of pseudomonas species using blochip technology. Sequences ABO67826-components for aeruginosa polypeptides of the printed sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                               Gaps
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Pred. No. 3.9e+03;
0; Mismatches 8; Indels
                                        Score 19; DB 8; Length 323; Pred. No. 3e+03; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 23285; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                     Pseudomonas aeruginosa polypeptide #6714.
                                                                                                                                                                   ABO74539 standard; protein; 442 AA.
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33.3%;
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                                          Query Match 95.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity 33.3%
Lange 4; Conservative
                                                                                                            270 RRSAARASRTAR 281
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                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
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                   Sequence 323 AA;
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invention.
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Peyman JA;
, Stone DJ;
Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic; hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV53; protein-kinase-like protein; chromosome 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides or polynucleotides, useful for preventing or treating disorders or syndromes e.g., atherosclerosis, hypertension, obesity or cancer.
                                                                                                                                                                                                                                                                   2001US-0271840P.
2001US-0272404P.
2001US-0272410P.
2001US-0272414P.
2001US-0272414P.
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2001US-0280039P.
2001US-0280818P.
2001US-0283443P.
2001US-0285754P.
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                                                                                                                             WO200268652-A2.
                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2001;
02-MAR-2001;
02-MAR-2001;
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16-MAR-2001;
20-MAR-2001;
20-MAR-2001;
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30-MAR-2001;
02-APR-2001;
                                                                                       Homo sapiens
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23-APR-2001;
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31-MAY-2001;
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13-AUG-2001;
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                                                                                                                                                                       06-SEP-2002
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Gaps

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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                            Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 738-739; 765pp; English.
                                                                                AAU33234 standard; protein; 644 AA.
                                                                                                                                                                                  Novel human secreted protein #3725.
                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US008656.
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26-JAN-2001; 2001US-00770160.
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56 RRARAATSRAAR 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-611725/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 644 AA;
                                                                                                                                                                                                                                                                                                                   WO200179449-A2
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                  18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001
                                                                                                                 AAU33234;
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                                                                 AAU33234
ID AAU
                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding retinal protein sNETO1, useful for diagnosis of retinal disease, especially macular degeneration, also for drug screening
                                              The present invention relates to novel human NOVX proteins, where X is any number from 1 to 91 and their coding sequences. The proteins and coding sequences are useful for preventing or treating disorders or syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV53 is a protein kinase-like protein and its coding sequence maps to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; retina-specific protein; NETO1; retinal disease;
age related macular degeneration; night blindness; protein kinase A203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retina-specific protein - NETO1. The DNA and protein sequences of the invention are useful in the treatment of retinal diseases, such as macular degeneration (especially age related) and night blindness. The present amino acid sequence represents human retina-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequences of a human
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                                                                                                                                                                                                Score 19; DB 5; Length 533; Pred. No. 4.5e+03; 0; Mismatches 8; Indels
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33.3%; Pred. No. 4.5e+03;
ive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human retina-specific protein kinase A203.
                                                                                                                                                                                                                                                                                                                                                                                     ADG48250 standard; protein; 534 AA.
                 Claim 1; Page 298; 923pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LYNK-) LYNKEUS BIO TECH GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2002; 2002EP-00003675.
21-FEB-2002; 2002US-0357857P.
                                                                                                                                                                                                    95.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2003; 2003WO-EP001625
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                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                    56 RRARAATSRAAR
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N-PSDB; ADG48249.
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Best Local Similarity
                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                   Sequence 533 AA;
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                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                    Matches
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the interior states to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying a therapeutic agent identifying apents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins to result as untritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation, as anti-inflammatory agents; and in treatment of leukaemias. AMU25910-AMU3304 represent the amino acid sequences of novel human expressions.
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The invention relates to novel human secreted polypeptides. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP76678 standard; protein; 19938 AA.
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3 RRXXXXXXXX 14

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immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra - Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for the treatment of sepside and the detection and removal of endotoxins. The peptides of the invention are used in a method for detecting endotoxin in a sample comprising contacting the sample with a labelled helix peptide endotoxin in a sample which comprises exposing the sample of removing condotoxin. The peptides can also be used in a method for removing endotoxin in a sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from which new analogues may be designed. This sequence represents the peptide Arg Helix #3 which is used in the method of the invention
                                                                                                                                                                                                                                                                              Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sepsis; branched chain peptide; antibacterial; immunosuppressive; endotoxin; helix peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Ala is modified by unidentified R1 group"
                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel use of antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 5; I
Pred. No. 4.9e+02;
0; Mismatches 8;
                                                                                                                                                          (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide Tris-Arg Helix #3 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB71430 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 2, 18pp; English
                                                                                                                                                                                                    Wolz G;
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                                                                            14-FEB-2002; 2002EP-00251027
                                                                                                                      14-FEB-2001; 2001US-0268410P
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ilarity 33.3%;
Conservative
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                                                                                                                                                                                                    Wolz RL,
                                                                                                                                                                                                                                          WPI; 2002-659478/71
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
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Modified-Bite
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EP1232754-A2
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                                        21-AUG-2002
                                                                                                                                                                                                    Harris RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
                                                                                                   Avilamycin, antibacterial, virucide, protozoacide, fungicide, infection, medicine, Staphylococcus aureus, biosynthetic gene cluster, enzyme.
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(CH2)3-Tris-ArgHel#3, where the Tris-ArgHel#3 is
represented in AAB71431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                             Streptomyces viridochromogenes Avi gene cluster polypeptide frame 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New avilamycin derivatives, useful for treatment of infections, and
nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sepsis; branched chain peptide; antibacterial; immunosuppressive; endotoxin; helix peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 6; Length 19938;
Pred. No. 7.6e+04;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide Arg Helix #3 for construction of Tris-Arg helix #3.
                                                                                                                                                                                                                                                                                                                                                                                                             Bechthold A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Acylated residue"
                                                                                                                                                                                                                                                                                                                                                                                                             Trefzer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 68-301; 319pp; German
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                                                                                                                                                                                                                                                                                                                                                                     (COMB-) COMBINATURE BIOPHARM AG.
                                                                                                                                                                Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-EP009815.
                                                                                                                                                                                                                                                                                                                                 25-FEB-2001; 2001DE-01009166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11248 RRRSSTASRTSR 11259
                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19938 AA;
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                                                                                                                                                                                                           WO200268436-A1
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Modified-site
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                         26-FEB-2003
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ABZ37516)

Synthetic.

AAB71432;

AAB71433

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Gape

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Length 15;

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mammal by reducing the anticoagulant effects of heparin.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB71428;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                           This invention describes a novel use of antibacterial and immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra - Arg Helix 3 for the manufacture of a medicament for the treatment of sepsis and the detection and removal of endotoxins. The peptides of the invention are used in a method for detecting endotoxin in a sample comprising contacting the sample with a labelled helix peptide cand then detecting the presence of any labelled molecule bound to endotoxin. The peptides can also be used in a method for removing endotoxin in a sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The candotoxin removal may be in vivo, or the peptides may be used to form an affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from which new analogues may be designed. This sequence represents the peptide Arg Helix #3 which is used in the construction of Tris-Arg Helix #3, a branched chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heparin binding peptide; antagonist; cardiovascular; coagulant; bleeding wound; vascular anastomoses; leaking prosthetic vascular graft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New heparin binding molecules, useful for reducing heparin content in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                        Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
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Pred. No. 5.2e+02;
); Mismatches 8; Indels
                                      (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heparin binding peptide Bis-Arg helix #2.
                                                                                                                                                                                                 Disclosure; Fig 1B; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%;
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   14-FEB-2001; 2001US-0268410P
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                                                                         Wolz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4, Conserva
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                                                                                                           WPI; 2002-659478/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                         Harris RB,
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This invention describes novel heparin binding molecules (I). The molecules (I) are useful as heparin ancagonist drugs for cardiovascular application and specifically neutralize heparin's conventional anticoagulant properties. (I) are also useful for counteracting actions of heparin locally e.g. in bleeding wounds, vascular ansatomoses or leaking prosthetic vascular grafts. (I) is also useful combined in a pharmaceutical composition with insulin, as a substitute for protamine for use in treating diabetics. The heparin binding molecules (I) specifically neutralize heparin's conventional anticoagulant properties without causing deleterious hemodynamic side-effects or exacerbation of the proliferative vascular response to injury. (I) are short-duration, intravenous drugs to be used in elective or emergency situations which can safely and specifically neutralize heparin's proliferative response to injury. This sequence represents a heparin's proliferative response to injury. This sequence represents a heparin's broliferative response to injury. This sequence represents a heparin-binding peptide described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel use of antibacterial and immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for the treatment of sepsis and the detection and removal of endotoxins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sepsis, branched chain peptide, antibacterial, immunosuppressive; endotoxin, helix peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Ala is modified by unidentified R1 group"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 3; Len
Pred, No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide Bis-Arg Helix #2 fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB71428 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A; 18pp; English
Example 1; Fig 1a; 39pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-659478/71.
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Matches 4; Conserv
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peptides of the invention are used in a method for detecting endotoxin in a sample comprising the presence of any labelled molecule bound to endotoxin. The presence of any labelled molecule bound to endotoxin. The peptides can also be used in a method for removing endotoxin in a sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The addotoxin removal may be in vivo, or the peptides may be used to form an affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from which new analogues may be designed. This sequence represents the peptide Arg Helix #2 which is used in the construction of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABNIS762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; OREX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                    Score 18; DB 5; Length 19;
Pred. No. 5.9e+02;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX protein sequence SEQ ID NO:540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP00279 standard; protein; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
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33.3%;
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                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myasthenia gravis.
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                                                                                                                                                                                                                                                                     Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                          Query Match
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disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide squadeness can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psorlamis, benign tumours, keloid, degenerative disorders, haemorrhage, cstecarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases mellitus, systemic transplantation, cardiovascular diseases, miletius, systemic storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from rependence dare for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lightin production; plant growth regulator; yield; plant growth, plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct, useful for improving plant tolerance to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protectant; plant growth regulant; gene therapy; plant;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 59;
                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 5; Length 59;
Pred. No. 1.4e+03;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant full length insert polypeptide segid 45271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADX75905 standard; protein; 64 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                                                                                                                                                                         33.3%;
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ZHOU Y.
KOVALIC D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-180133/17.
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TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein content
                                                                                                                                                                                                                                                                                                                                                           Sequence 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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(CAOY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KOVA/)
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Example 1; SEQ ID NO 3113; 1069pp; English.

treating acne vulgaris.

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, hear, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing gladactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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, Jen S, Carter D;
                                                                         Claim 1; SEQ ID NO 45271; 15pp; English.
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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s J, Zhang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001.
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for

WPI; 2001-616774/71.

N-PSDB; AASS9515

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by each acrea and cardendes of medical conditions caused by proteins. The disorders include SAPHO syndrome (synovitis, acne, parens), hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessions associated with acnes via apatient comprises contacting a mapper by a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to convergulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins of the sample, by cansyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 4; Length 77; Pred. No. 1.8e+03; 0; Mismatches 8; Indels
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Similarity 33.3%;
4; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
셤
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 29, 2006, 01:44:43 ; Search time 20.5625 Seconds (without alignments) 65.509 Million cell updates/sec

1 XXRRXXXXXXXXX 14 US-10-712-447-210 20 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ч		pr	cyaE protein - Bor	hABC transport pro	hypothetical prote		cvgSy protein (AE0	hypothetical prote	hypothetical prote	splicing factor, a	hypothetical prote	probable transposa	hypothetical prote	spliling factor SR	hypothetical prote	hypothetical prote	probable proteinas		probable PHD-type	hypothetical prote	probable calcium c	probable potassium	hypothetical prote	DNA (cytosine-5-)-	hypothetical prote		sperm chromatin pr
DB ID	2 \$65036	2 JH0404	2 T30752	2 T18918	1 BVBRCE	2 T14162	2 D72453	2 AI3144	2 B98143		2 D87267	2 A57198	2 G70705	2 T29423	2 PQ0339		2 E82796	2 T36706		2 E87435	2 T40911			2 T31354	2 T19722	_	2 G71415	2 A46068	2 PN0081
Length [79	79	110	197	474	574	099	668	710	1.95	207	238	241	310	317	344	395	436	461	520	571	717	724	1017	1577	1622	2351	3144	25
Query	90.06	90.0	90.0	0.06	0.06	90.0	90.0	90.0	90.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	80.0
Score	18	18	18	18	18	18	18	18	18	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	16
Result No.	-	8	וח	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

hypothetical prote protamine Pi - duc	nucleocapsid prote ribosomal protein	30S ribosomal prot 30S ribosomal prot	late embryogenesis	ribosomal protein	sperm protein EM6	hypothetical prote	hypothetical prote	protein limported	hypothetical prote	hypothetical profe	pIL2 hypothetical	hypothetical prote
E86930 S39425	VHNVBM A82875	AC2616 B97398	S29941	G87249	\$21225	F72785	D71162	C95386	B72683	T14796	A26882	G75510
0 0	7	2 0	N	~	0	7	~	~	7	~	~	7
57	65 79	88 8	8 6	91	101	125	126	139	142	144	175	184
80.0	80.0 80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
16 16	16 16	16	19	16	16	16	16	16	16	16	16	16
30 31	32	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 855036 nuclear basic protein SP4, sperm-specific - African class 55036 nuclear basic protein SP4, sperm-specific - African classed frog) C;Species: Xenopus laavis (African classed frog) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #tex C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #tex C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #tex C;Atta, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagi Biochim. Biophys. Acta 1245, 430-438, 1995 A;Title: Structure of genes for sperm-specific nuclear A;Feference number: S65036, MUID:96125743; PMID:8541323 A;Accession: S65036 A;Molecule type: DNA A;Residues: 1-79 eMIT> A;Residues: 1-79 eMIT> A;Residues: 1-79 eMIT> A;Gross-references: UNIPARC:UPIO00017BF96; EMBL:D45253 A;Gross-references: UNIPARC:UPIO00017BF96; EMBL:D45253 A;Genetics: A;Genetics: A;Genetics: A;Alntrons: 76/1	RESULT 1 S65036 nuclear basic protein SP4, sperm-specific - African clawed frog nuclear basic protein SP4, sperm-specific - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997 C;Date: S0-Oct-1996 #sequence_revision 13-Mar-1997 R;Mita. K; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C. Biochim. Biophys. Acta 1245, 430-438, 1995 A;Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus la A;Recession: 865036 A;Eterence number: S65036, MUD:96125743; PMID:8541323 A;Accession: 865036 A;Status: preliminary A;Residues: 1-79 eMIT> A;Residues: 1-79 eMIT> A;Residues: 1-79 eMIT> A;Cross-references: UNIRARC:UPI000017BF96; EMBL:D45253 A;Cross-references: UNIRARC:UPI000017BF96; EMBL:D45253 A;Cross-references: UNIRARC:UPI000017BF96; EMBL:D45253 A;Gene: XLSP41 A;Introns: 76/1	n Xenopus la
Query Match Best Local Similarity 33.3 Matches 4; Conservative	Query Match Best Local Similarity 33.3%; Pred. No. 46; Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps	0;

45 RRARTSTARRAR 56 3 RRXXXXXXRX 14

Š a RESULT 2

Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Cipacesion: JH04004; PU0021; \$65037; \$55038; \$65039
R.Hiyoshi, H.; Uno, S.; Yokota, T.; Katagiri, C.; Nishida, H.; Takai, M.; Agata, K.; Egu Exp. Cell Res. 194, 95-99, 1991
A.jritle: Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and A.Reference number: JH04004; MUID:91200205; PMID:2015853 A,Molecule type: mRNA A,Residues: 1-79 https://documer.org/line-references: UNIPROT: P24056; UNIPARC: UPI0000000506; GB: D00916; NID: 9222970; PIDN A,Experimental source: round spermatid A,Accession: PU0021

A;MOLOCULE type: protein
A;Residues: 2-11;12-43;65-74;75-79 <HIZ>
A;Residues: 2-11;12-43;65-74;75-79 <HIZ>
A;Cross-references: UNIPARC:UP1000017BF78; UNIPARC:UP1000017BF79; UNIPARC:UP1000017BF7A, R;Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.
Biochim. Biophys. Acta 1245, 430-438, 1995
A;Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus 1-A;Reference number: S65036; MUID:96125743; PMID:8541323

Wed Mar 29 18:01:20 2006

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A;Molecule type: DNA
A;Residues: 1-474 <GLA>
A;Cross-references: UNIPROT:P11092; UNIPARC:UP1000012889E; EMBL:X14199; NID:g39731; PIDN:
C;Comment: This protein is required for the transport of cyclolysin (or calmodulin-sensit
lease into the external medium. This secretion process is very similar to that of the E.
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C;Date: 20-8ep-1999 #sequence_revision 20-8ep-1999 #text_change 09-Jul-2004
C;Accession: T14162
R;Yu, S.; Fiss, B.; Jacobs Jr., W.R.
A;Title: Analysis of the exochelin locus in mycobacterium smegmatis: biosynthesis genes }
A;Reference number: Z17898; MUID:98389687; PMID:9721311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT:087312; UNIPARC:UPI00000B60F3; EMBL:AF027770; NID:g3560502; I
C; Superfamily: Streptomyces glaucescen ABC transporter strV; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ridaser, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin, A. EMBO J. 7, 3997-4004, 1988
A/ittle: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase--haemolysin A, Reference number: $02386; MUID:89091151; PMID:2905265
A, Accession: $02388
                                                                                                                                                                                                                                                                                    A:Readides: 1-197 - WIL->
A:Readides: 1-197 - WIL->
A:Cross-references: UNIPROT:Q17626; UNIPARC:UPI000007ED49; EMBL:Z70718; PIDN:CAA94670.1;
A:Experimental source: clone C04G2
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hypothetical protein C04G2.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Bordetella pertussis
C.Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C.Accession: S02388
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Pred. No. 2.2e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hABC transport protein homolog - Mycobacterium smegmatis
                                                                                                                      R;Hembry, C.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z19045
A;Accession: T18919
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T14162, A; Accession: T14162, A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 2;
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: cyclolysin transport; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyaE protein - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Matches 4; Conservative
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C;Superfamily: cyaE protein
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                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
A, Gene: CESP: C04G2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      position: 4
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BVBRCE
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Nypothetical protein 150R - Molluscum contagiosum virus 1

NyAlternate names: MC150R

C;Species: MOlluscum contagiosum virus 1

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T30752

R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

SGience 273, 813-815, 1996

A;Title: Genome sequence of human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: 220876; MUID:96325459; PMID:8670425

A;Accession: T30752

A;Accession: T30752

A;Accession: T30752

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-110 <SEN>

A;Residues: 1-110 <SEN>

A;Cross-references: UNIPROT:Q98316; UNIPARC:UP100000ECB2C; EMBL:U60315; NID:g1491943; PI

A;Gonetios: MC150R
                                 A; Molecule type: DNA
A; Residues: 1-79 < MIT>
A; Residues: 1-79 < MIT>
A; Residues: 1-79 < MIT>
A; Cross-references: UNIPARC:UPI000000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PI
A; Experimental source: strain J
A; Genetics: CH
A; Mote: the authors translated the codon TAT for residue 73 as Thr
A; Molecule type: DNA
A; Residues: 1-79 < MIS>
A; Cross-references: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PI
A; Experimental source: strain J
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A,Residues: 1-79 AMIW>
A,CTOSS: Teferences: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PI
A,Experimental source: strain J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genetics: CH3
A;Note: the authors translated the codon TAT for residue 73 as Thr C;Genetics: <CH1>A;Gene: XLSP42
                                                                                                                                                                                                                                                                                                                                                              A;Genetics: CH2
A;Note: the authors translated the codon TAT for residue 73 as Thr
A;Accession: S65039
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Pred. No. 46;
0; Mismatches
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Best Local Similarity 33.3.
A; Conservative
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Best Local Similarity
            A; Accession: S65037
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C; Genetics: <CH2>
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C;Genetics: <CH3>
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ð g Matches

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hyportetical protein APB0999 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72697
C;Accession: G72697
R;Kawarabayasi, Y:; Hino, Y:; Horikawa, H:; Yamazaki, S:; Haikawa, Y:; Jin-no, K:; Takah awa, H:; Takamiya, M:; Masuda, S:; Funahashi, T:; Tanaka, T:; Kudoh, Y:; Yamazaki, J:; K)
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn
A;Reference number: A72450; MUID:99310339; PMID:10382966
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87267
E;Accession: D87267
B;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon, D.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q8U6M6; UNIPARC:UPI0000D26D3; GB:AE007870; PIDN:AAK88668.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 710;
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Pred. No. 3.1e+02;
0; Mismatches 8; Indel8
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33.3%; Pred. No. 2.1e+02;
iive 0; Mismatches 8;
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A;Map position: linear chromosome
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Matches 4; Conservative
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-710 < KUR>
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A,Status: preliminary
A,Molecule type: DNA
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                              Wypotherical protein APE2272 - Aeropyrum pernix (strain K1)
C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Species: Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C,Accession: D72453
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takanhya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaference number: A3-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72453
A;Accession: D72453
A;Accession: D72453
A;Accession: DNA
A;References: UNIPACT:Q9Y9L6; UNIPARC:UPI000005E2A0; DDBJ:AP000064; NID:G5105945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          two component sensor kinase Atu4781 [imported] - Agrobacterium tumefaciens (strain C58, C; Species: Agrobacterium tumefaciens (cjpacies: Agrobacterium tumefaciens (cjpacies: Agrobacterium tumefaciens (cjpacies: 11-3an-2002 #sequence_revision 11-3an-2002 #text_change 09-Jul-2004 C; Accession: Al3144 B; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R; Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karsenco, P.; Romerco, P.; Zhang, S. Science 294, 2317-2323, 2001 B; Ahathbors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Accession: A13144

A;Status: preliminary

A;Molecule type: DNA

A;Coss-references: UNIPROT:O8UGMG; UNIPARC:UPI00001649AC; GB:AE008689; PIDN:AAL45575.1;

A;Experimental source: strain C58 (Dupont)

A;Genetical

A;Map position: linear chromosome
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     Length 574;
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Score 18; DB 2; 1
Pred. No. 2.6e+02;
0; Mismatches 8;
  Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
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                                                                                                                                                                       233 RRALTATLRAAR 244
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A; Experimental source: strain H37Rv
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BMBO J. 13, 2639-2649, 1994
A;Title: Characterization and cloning of the human splicing factor 9G8: a novel 35 kDa fa;Reference number: S46319; MUID:94283389; PMID:8013463
A;Reference number: S46319
A;Accession: S46319
A;Accessi
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(970705
hypothetical protein Rv0756c - Mycobacterium tuberculosis (strain H37RV)
(5)Species: Mycobacterium tuberculosis
(5)Date: 17-010-1998 #sequence_revision 17-Ju1-1998 #text_change 09-Ju1-2004
(5)Accession: G70705
(5)Accession: G70705
(6)Accession: G70705
(7)Accession: G70705
(8)Accession: G70705
(8)Accession
               A,Residues: 1-207 <STO>
A,Rores references: UNIPROT:Q9ABS1; UNIPARC:UPI0000CGF4E; GB:AE005673; NID:g13421262;
C,Genetics:
A,Gene: CC0149
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              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Pred. No. 2.2e+02;
0; Mismatches 8; Indels
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A;Cross-references: GDB:378350; OMIM:600572
A;Map position: 2022-2021
A;Introns: 10/1; 70/2; 129/2; 154/2; 191/2; 209/2; 221/2
F;12-74/Domain: ribonucleoprotein repeat homology <RRM3>
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A;Molecule type: DNA
A;Residues: 1-238 <RES>
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A;Residues: 1-310 <PAR>
A;Cross-references: UNIPROT:O86606; UNIPARC:UPI0000DAD10; EMBL:AL031155; NID:e1313489; E
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 317 - Lymantria dispar nuclear polyhedrosis virus (fragment)
N'Alternate names: ORFA protein
C'Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV
N'R R'Bjornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A'Fitle: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymant
A'Reference number: PQ0339; MUID:92300345; PMID:1607868
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29423
R;Parkhill, J:; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: 220619
A;Accession: T29423
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.0%; Score 17; DB 2; Length 317; 33.3%; Pred. No. 3.2e+02; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 33.3%; Score 17; DB 2; Length 310; Similarity 33.3%; Pred. No. 3.2e+02; 4; Conservative 0; Mismatches 8; Indels
   Length 241;
85.0%; Score 17; DB 2; Length 241
33.3%; Pred. No. 2.6e+02;
ive 0; Mismatches 8; Indels
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A,Molecule type: DNA
A,Residues: 1737 < 6JJO>
A,Cross-references: UNIPARC:UPI000017A7C2; DDbJ:D10836
                                                                                                                                                                                                                                                                                                                                                    probable transposase - Streptomyces coelicolor
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                                                                                           (without alignments)
76.532 Million cell updates/sec
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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Q7RWX1_NEUCR
Q965V1_CAEEL
Q4SDD4_TETNG
Q74EXQ_GEOSL
Q7FOMZ_ORYSA
Q4LNR3_9BURK
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PERQI HUMAN
Q4QE71 LEIMA
Q4NSL6 9DELT
Q5N831 ORYSA
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VCO7_ADEB2
Q7M6E8_ADEB2
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SP4 XENLA
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=2CP-C;
STRAIN=2CP-C;
US DOS Joint Genome Institute (JGI-ORNL);
Latimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEWBLrel. 31, Created)
13-SEP-2005 (TrEWBLrel. 31, Last sequence update)
13-SEP-2005 (TrEWBLrel. 31, Last annotation update)
ATP-binding region, ATPase-like:Histidine kinase A, N-terminal
          QBIhv7 c
Q63x19 h
Q5y8d5 i
Q528d5 i
Q828f5 i
Q8rjr6 i
Q9rjr6 i
Q5w6d52 c
Q5w6d52 c
Q4nc22 i
Q4lpk5 h
Q4lq72 g
Q4lq72 g
Q4lq72 g
                                                                                                                                                                                                                                                                                                                                              ORFNames=AdehDRAFT_3131;
Anacromysobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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414 AA; 41594 MW; OADFOFODCAOBOC53 CRC64;
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AC QTRWXI NEUCR PRELIMINARY; PRT; 452 AA.

DT 01-WAR-2004 (TrEMBLrel. 26, Created)

DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
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Pred. No. 2.6e+02;
); Mismatches 8;
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EMBL, AAHDUInnary data.

EMBL, AAHDUInnary data.

ATP-binding, Kinase, Signal.

1 32 ATP-binding.
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                                                           QSB410 EMENI
Q9RJR6 STRCO
Q6EQ52 ORYSA
Q5W6D5 ORYSA
Q4NTZ2 9DELT
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Q4LPK5 9BURK
Q4IQ72 GIBZB
CYAE BORPE
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              ORYSA
                                     NOCFA
                                                                                                                                                               O7W1M9 BORPA
Q7EYP7_0
Q8LHV7_0
Q63X19_B
                                  QSYSDS_N
Q828F2_S
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NUCLEOTIDE SEQUENCE
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Mismatches
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OrderedLocusNames=GSU0839;
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33.3%; P
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Q4SDD4;
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Best Local Similarity 33...
4. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q74EX0 GEOSL PRELIMINARY;
                                                                         595 RRATSTITISE 606
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 4; Conservative
                                    3 RRXXXXXXXX 14
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Matches
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                                                                                                                                  RESULT 4
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                                                                                                                                                                                 Adalagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bitins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Oui D., Ianakiev P., Redersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roche G.O., Jedd G., Mewsey W., Staben C., Marcotte E., Greenberg D., Ramal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Maulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Natue O:O. (2003).

Nature O:O. (2003).

Intre Genome Sequence of the Filamentous Fungus Neurospora crassa.";

Nature O:O. (2003).

ENBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                  Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MDDLINE=99069613; PubMed=9851916;
The Clegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
BML; ACO24/94; AAK68497.1; -; Genomic DNA.
Ensembl; Y48G1BM.5; Caenorhabditis elegans.
Wormbase; WRGene0021670; Y48G1BM.5.
Wormbase; WRGAGBM.5; CE26117.
InterPro; IPR008266; Tyr pkinase_AS.
PROSITE; PS00109; PROFENT KINASE_TYR; UNKNOWN_1.
COMplete proteome; Hypotherical protein.
SEQUENCE 994 AA; 111289 MW; 73F6FG32D71D5CCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
1, AABX01000758; EAA27000.1; -; Genomic_DNA.
ENCE 452 AA; 47319 MW; F1737BB5A3111CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Hypothetical protein Y48G1BM.5.
ORFNames=Y48G1BM.5;
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 2;
Pred. No. 2.8e+02;
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Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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33.3%; P
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Q965V1;
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Best Local Similarity
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                     Predicted protein.
Name=NCU08793.1;
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EMBL;

Matches

RESULT 3

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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Auillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Andraud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Anthouard V., Jahin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Rellis M., Volff JW., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
"The early vertebrate proto-karyotype.";
Hattre 431:946-957(2004).
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                                                       M.2.2.,
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome as SCAFIA639, whole genome shotgun sequence.
ORRNames=GSTENG00120093001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontoidea; Tetraodontidae; Tetraodon.
MCBL_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenEank/DDBJ whole genome shotgun (WGS) entry whic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 2; Length 11 Pred. No. 7.4e+02; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAB01014639; CAG01348.1; -; Genomic_DNA.
iCE 1139 AA; 121432 MW; 7E2BD59621B51FCC CRC64;
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Last annotation update)
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PRT; 1139 AA.
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oreliminary data
                                                                                                               NUCLEOTIDE SEQUENCE.
[1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                             Oxidoreductase.
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Q8DI46;
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                   Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.H., Pelablyum T.V., Utterback T.R., Wan Aken S.E., Lovley D.R., Fraser C.M.,
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames=Bcen2424DRAFT 2557;
Burkholderia cenocepacia H12424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 2; Length 214; 33.3%; Pred. No. 2.7e+02;
                                                                                                                                                                                              Score 19; DB 2; Length 194;
Pred. No. 2.5e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last amnotation update)
Delta 1-pyrrolline-5-carboxylate reductase (EC 1.5.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA; 23349 MW; E106D482D50E50C0 CRC64;
                                                                                                                                                                        21055 MW; DOBOD918D3F2CACB CRC64;
                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein P0450A04.111.
             PubMed=14671304; DOI=10.1126/science.1088727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                        EMBL; AE017180; AAR34169.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP004274; BAC83398.1; -; Genomic_DNA
                                                                                                                                                              Complete proteome; Hypothetical protein. SEQUENCE 194 AA; 21055 MW; D0B0D918L
                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                95.0%;
33.3%;
                                                                                                                            Science 302:1967-1969(2003).
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Q4LNR3;
                                                                                                                                                                                     Query Match
Best Local Similarity 33.3-
4; Conservative
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Q7F0M2;
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   STRAIN=PCA / ATCC 51573;
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Best Local Similarity
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                                                                                                                                                     GSU0839; -.
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                                                                                                                    environments."
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Yaa-, in which Xaa is preferably Leu, but may be other amino acid
including Pro although not Arg or Lys, and Yaa may be Pro. Amino
acid amides and methyl esters are also readily hydrolyzed, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
MARAMURA Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Res. 9:123-130(2002). Proceeding and regular Proversions. Perunaver of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rates on arylamides are exceedingly low.
--- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
--- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the peptidase M17 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 444;
                                                                                                                                                                                                                                                                                            STRAIN=HI2424;
US DOB Joint Genome Institute (JGI-ORNL);
Liarimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia (HI2424,")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 AA; 47128 MW; 6219556CF63899C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 2; 333.3%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AAHL01000036; EAM17718.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
11-OCT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
12-bable cytosol aminopeptidase (EC 3.4.11.1)
(LAP) (Leucyl aminopeptidase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 RRATRAASRTAR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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 DOMAIN
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Matches
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as long as its content is in no way modified and this statement is not
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,

Taui L.-C., Rosenthal A.;

"Large-scale sequencing of two regions in human chromosome 7q22:
analysis of 500 kb of genomic sequence around the EPO and CUTL1 loci
reveals 17 genes.";

Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                          potential.
264 Manganese 2 (By similarity).
267 Manganese 1 and 2 (By similarity).
268 Manganese 1 (By similarity).
369 Manganese 1 (By similarity).
360 Manganese 1 (By similarity).
361 Manganese 1 and 2 (By similarity).
                                             MESDPS; M17.002; -.

MESDPS; M17.002; -.

HAWAP; MF.00181; -.

InterPro; IPR018135; Peptidase_M17.

InterPro; IPR00819; Peptidase_M17.

InterPro; IPR008819; Peptidase_M17.

Pfam; PF00881; Peptidase_M17, 1.

Pfam; PF00881; Peptidase_M17, 1.

PFRSF; PIRSF001116; Ctsl_ammpptdse; 1.

PRNSF; PRSF001116; Ctsl_ammpptdse; 1.

PRNSF; PRSF001116; Ctsl_ammpptdse; 1.

Amnopeptidase; Complete proteome; Hydrolase; Manganese; Mart_all-binding; Protesse.

PACT_SITE 351 351 Potential.
                                                                                                                                                                                                                                                                                                                              Length 497;
                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                              Score 19; DB 1; I
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FSP-2005 (Rel. 48, Last annotation update)
PERQ amino acid rich with GYF domain protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      817 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF053356; AAC78792.1; -; Genomic_DNA
Ensembl; ENSG00000146830; Homo sapiens.
                                    EMBL; BA000039; BAC09297.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reveals 17 genes.";
Genome Res. 8:1060-1073(1998).
-!- SIMILARITY: Contains 1 GYF domain.
                                                                                                                                                                                                                                                                                                                              95.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC, HGNC:9126; PERQ1.
InterPro; IPR003169; GYF.
Pfam; PF02213; GYF; 1.
SMART; SM00444; GYF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       93 RKTAATIAKTAK 104
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264
269
287
287
347
349
497 AA;
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nes 4; Conserv
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075420;
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                                                                                                                                                                                                                                                                                                     SEQUENCE
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PROSITE, PS50829; GYF; 1

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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S., Sunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases. EMBL, TC005256; CAJ03330.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 833 AA; 87127 MM; 7P8BD43D0F4C2256 CRC64;
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US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C."; to the EMBL/GenBank/DDBJ databases.
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Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
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Pred. No. 1.2e+03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                      Length 817;
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Pred. No. 1.1e+03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                      Polý-Gln.
C727AD2E7C2E2581 CRC64;
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Last annotation update)
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Last annotation update)
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                            Poly-Glu.
Poly-Gly.
Poly-Glu.
Gln-rich.
Poly-Pro.
Poly-Glu.
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
Hypothetical protein.
ORFNames=AdehDRAFT_1669;
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                                                                                                                                                                                                                                                                          89741 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 14) Phychetical protein. ORFNames=LmjF17.1200;
                                                                                                                                                                                                                                                                                                                                          95.0%;
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Q4NSL6;
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Q4QE71 LEIMA PRELIMINARY;
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Best Local Similarity 33...
4; Conservative
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les 4; Conservative
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260
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                                                                                                                                                                                                                                          751 .
817 AA;
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ID Q4NSL6 97
A 13-SEP-20
DT 13-
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Query Match

SARAFTACCORRES

ORYSA

RESULT 12 QSN831_ORY

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MEDLINE=96125743; PubMed=8541323; DOI=10.1016/0304-4165(95)00124-7;
Mita K., Ariyoshi N., Abe S., Takamune K., Katagiri C.;
"Structure of genes for sperm-specific nuclear basic protein (SP4) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Round spermatid;
MEDLINE=91200205; PubMed=2015853;
Hiyoshi H., Uno S., Yokota T., Katagiri C., Nishida H., Takai M.,
Agata K., Eguchi G., Abe S.-T.;
"Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and evidence for expression of SP4 mRNA in primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spermatocytes.";
Exp. Cell Res. 194:95-99 [1991).
Exp. Cell Res. 194:95-99 [1991).
-!- DEVELOPMENTAL STAGE: SP4 gene is transcribed in or before primary
-!- DEVELOPMENTAL STAGE: AP4 gene is transcribed in or before primary
spermatocyte stage but is translated at the round spermatid stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Sperm-specific nuclear basic protein (SP4).
Name-XLSP43; Synonyms-XLSP42, XLSP44;
Racpus lacvis (African clawed frog).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosto
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-43 AND 64-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct protein sequencing; Nuclear protein; Repeat; Sperm.
INIT MET 0 0
REPRAT 44 51
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Biochim. Biophys. Acta 1245:430-438(1995).
EMBL; D45253; BAA08210.1; -; Genomic_DNA.
EMBL; D45253; BAA08211.1; -; Genomic_DNA.
EMBL; D45253; BAA08209.1; -; Genomic_DNA.
SEQUENCE 79 AA; 9325 MW; 920C021D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;
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Pred. No. 2e+02;
0; Mismatches
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Sperm-specific basic nuclear protein SP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 A.
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                                                                                                                                                                                                           Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D00916; BAA00762.1; -; mRNA. PIR; JH0404; JH0404.
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                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus; Xenopus
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33.3%;
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Q53X49;
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es 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                        Name=SP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2005 (TYEMBLrel. 29, Created)
01-FEB-2005 (TYEMBLrel. 29, Last sequence update)
01-FEB-2005 (TYEMBLrel. 29, Last sequence update)
Hypochetical protein B1095003.55.
Name=B1095003.55;
Oryza sativa (japonica cultivar-group).
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                    Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
"Annotation of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
Submitted (UNT-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Nature 420:312-316(2002).
EMBL; AP003431; BAD82385.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 2; Length 856; 33.3%; Pred. No. 1.2e+03; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 2; Length 57;
Pred. No. 1.5e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.

EMBL; AAHD01000021; EAL78630.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 856 AA; 89899 MW; F33C3D7D3B663665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 AA; 6587 MW; 7A9814F81F280924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AA
                                                                                               STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
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Similarity 33.3%;
4; Conservative
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QSN831;
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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78 AA.

PRT;

STANDARD;

SP4 XENLA P24056;

RESULT 13 SP4_XENLA

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Gaps

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Length 78; 8; Indels

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MEDLINE=22803265; PubMed=12923100;
DOI=10.1128/JB.185.17.5269-5274.2003;
DOI=10.1128/JB.185.17.5269-5274.2003;
Stecker C. Johann A., Herzberg C., Averhoff B., Gottschalk G.;
"Complete nucleotide sequence and genetic organization of the 210-
kilobase linear plasmid of Rhodococcus erythropolis BD2.";
Kilobase linear plasmid of Rhodococcus erythropolis BD2.";
BHB1; AX223810; AAP73969-1; -; Genomic_DNA.
Hypothetical protein; Plasmid.
SEQUENCE 85 AA; 9111 MW; BB17D81B55DD0A2A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Nocardiaceae, Rhodococcus.
NCBI_TaxID=1833;
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90.0%; Score 18; DB 2; Length 85;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels
Query Match

90.0%; Score 18; DB 2; Length 79;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
08-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Rhydothetical protein.
Rhodococcus erythropolis.
Plasmid pBD2.
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OGXN62_RHOER PRELIMINARY;
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OGXN62_RHOER PRELIMINARY;
AC
OGXN62_RHOER PRELIMINARY;
AC
DT 05-JUL-2004 (TrEMBLrel. 27,
DT 05-JUL-2004 (TREMBLREL.
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Search completed: March 29, 2006, 01:49:13 Job time : 131.062 secs

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Sequence 8, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 2251, Appli
Sequence 21251, A
Sequence 24661, A
Sequence 24661, A
Sequence 23576, A
Sequence 23176, A
Sequence 21774, A
Sequence 21774, A
Sequence 21774, A
Sequence 2173, A
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Sequence 32376, A
Sequence 23285, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                            March 29, 2006, 01:49:32 ; Search time 29.3125 Seconds (without alignments) 39.487 Million cell updates/sec
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/jaa/5_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6_COMB.pep:*
/cgn2_6/ptodata/1/jaa/H_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
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US-09-252-991A-32376
US-09-252-991A-32385
US-08-660-592-11
US-09-166-930A-8
US-09-905-691-5
US-09-905-691-5
US-09-905-691-5
US-09-905-691-5
US-09-252-991A-32536
US-09-252-991A-32536
US-09-252-991A-325319
US-09-252-991A-325319
US-09-252-991A-37446
US-09-252-991A-37446
US-09-252-991A-37446
US-09-252-991A-37486
US-09-252-991A-37486
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                                                                                                                                                                                                                                 572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext
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1 XXRRXXXXXXXX 14
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seq length: 200000000
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Query
Match Length I
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Sequence 21789, A Sequence 18191, A Sequence 14078, A P Sequence 22531, A Sequence 22531, A Sequence 17459, A Sequence 17, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 20192, A Sequence 20192, A Sequence 20193, A Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
US-09-252-991A-21789
US-09-252-991A-18191
US-09-489-039A-9786
US-09-489-039A-9786
US-09-252-991A-25311
US-09-252-991A-17459
US-09-252-991A-17459
US-09-252-991A-17459
US-09-252-991A-17459
US-09-252-991A-17459
US-09-252-991A-1719
US-09-252-991A-3637
US-09-252-991A-3633
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RESULT 2
US-09-252-991A-32376

J Sequence 32376, Application US/09252991A

Sequence 32376, Application US/09252991A

RECORD SEQUENCE 32376

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT RAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

SEQ ID NOS: 33142

LENGTH: 189

TYPE: PRI

TYPE: PRI

  Sequence 21845, Application US/09252991A
Sequence 21845, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 95.0%;
Similarity 33.3%;
4; Conservative C
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Best Local Similarity
Matches 4; Conserv
US-09-252-991A-21845
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 133
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US-09-05-691-4

US-09-05-691-4

Sequence 4, Application US/09905691

Patent No. 6756206

GENERAL INFORMATION:

APPLICANT: Harris, Robert B.

APPLICANT: Wolz, Gabriella

TITLE OF INVENTYON: Adsorption and Removal of Endotoxin from Physiological

TITLE OF INVENTY PRILIGE

FILE REFERENCE: 006338-017

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

TENDOR: 1. TENDOR: 1.
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US-09-166-930A-8
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Pred. No. 1.1e+02;
0; Mismatches 8; Indels
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90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels
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US-09-166-930A-8

Sequence 8, Application US/09166930A

Sequence 8, Application US/09166930A

Patent No. 6200955

GENERAL INFORMATION:

APPLICANT: HARRIS, Robert B.

TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES

PILE REFERENCE: 006338-006

CURRENT APPLICATION NUMBER: US/09/166,930A

CURRENT FILING DATE: 1998-10-06

PRIOR PELIANG DATE: 1996-06-11

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 16
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FEATURE:
OTHER INFORMATION: Tris-Arginine Helix #3
                 TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
(703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    h 90.0%;
Similarity 33.3%;
4; Conservative
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                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide US-08-660-592-11
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Best Local Similarity
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Sequence 21285, Application US/09252991A

Patent No. 651795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PAPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 442
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                                                                            Length 189;
                                                                                                                       8; Indels
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Sequence 11, Application US/08660592

Sequence 11, Application US/08660592

Sequence 11, Application US/08660592

SEGNERAL INFORMATION:
APPLICANT: HARRIS, Robert B.
APPLICANT: HARRIS, Michael
TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
COUNTRY: United States
ZIRTE: 22313-146 FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PARABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PARABALE FORM:
MEDIUM SYSTEM: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,592
FILING DATE: 11-010-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McGOWAN, Malcolm K.
REGISTRATION NUMBER: 39,300
REFRENCE/DOCKET NUMBER: 066338-001
TELECOMMUNICATION INFORMATION:
                                                                          Score 19; DB 2;
Pred. No. 4.2e+02;
                                                                                                                          0; Mismatches
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32376
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ORGANISM: Pseudomonas aeruginosa
                                                                       Query Match 95.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity
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US-09-905-691-2
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                                                                                                                                                                                                                                                                             | Sequence 5, Application US/09905691
| Patent No. 6756206
| GENERAL INFORMATION:
| APPLICANT: Wolz, Robert B.
| APPLICANT: Wolz, Russell L.
| APPLICANT: Wolz, Gabriella
| TITLE OF INVENTION: Absorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Absorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Absorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Abuse Using Cationic Helix Peptides
| TITLE OF INVENTION: Abuse 1017
| CURRENT PILING DATE: 2001-02-14
| NUMBER OF SEQ ID NOS: 5
| SEQ ID NO 5
| SEQ ID NO 5
| LENGTH: 16
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                                           Length 16;
                                                                                      8; Indels
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CURRES FOUNDENCE ADDRESS:
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
CUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,592
FLING DATE: 11-UN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, MBICOLM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 006338-001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARRIS, Robert B.
APPLICANT: WARRIS, Michael
TITLE OF INVENTION: NOVEL HEARIN BINDING PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                      90.0%; Score 18; DB 2; 1 33.3%; Pred. No. 1.1e+02; iive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08660592; Sequence 10, Application US/08660592; Patent No. $877153; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                Best Local Similarity 33.2
Matches 4; Conservative
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US-09-905-691-4
                                           Query Match
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Sequence 3255, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: WUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32536
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CURRENT APPLICATION NUMBER: US/09/905,691
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 19
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Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismarchac
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Pred. No. 1.3e+02;
0; Mismatches 8;
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; Patent No. 6756206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32536
TELEPHONE: (703) 836-5620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10: 8EQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INPORMATION:
APPLICANT: Harris, Robert B.
APPLICANT: Wolz, Russell L.
APPLICANT: Wolz, Gabriella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RRAARAAARRAR 16
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                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-592-10
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US-09-252-991A-32536
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Sequence 24681, Application US/09252991A Patent No. 6551795
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Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-23676
US-09-252-991A-24681
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i Sequence 21251, Application US/09252991A

i Sequence 21251, Application US/09252991A

i Sequence 21251, Application US/09252991A

i Patent No. 6551795

j GENERAL INFORMATION:

i APPLICANT: Marc J. Rubenfield et al.

i APPLICANT: Marc J. Rubenfield et al.

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

i FILE REFERENCE: 107196.136

i CURRENT APPLICATION NUMBER: US 60/074,788

i PRIOR FILING DATE: 1999-02-18

i PRIOR FILING DATE: 1999-02-18

i PRIOR FILING DATE: 1999-07-27

i NUMBER OF SEQ ID NOS: 33142

i SEQ ID NO 21251
                                                                                                                                                                                                     RESULT 11
US-09-252-919A-17175
i Sequence 17175, Application US/09252991A
i Sequence 17175, Application US/09252991A
i Setent No. 6551795
i GENERAL INFORMATION:
i APPLICATION:
i TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i TILLE REPREBNE: 107196.136
i CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
i PRIOR PILING DATE: 1998-02-18
i PRIOR PILING DATE: 1998-02-18
i PRIOR FILING DATE: 1998-02-18
i PRIOR FILING DATE: 1998-02-18
i RIOR APPLICATION NUMBER: US 60/074,788
i PRIOR FILING DATE: 1998-07-27
i NUMBER OF SEQ ID NOS: 33142
i LENGTH: 1137
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Pred. No. 5.8e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
                     Length 103;
                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                   Score 18; DB 2; 1
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 2; 1
Pred. No. 5.1e+02;
0; Mismatches 8;
                                                             0; Mismatches
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US-09-252-991A-21251
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US-09-252-991A-17175
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                     33.3%;
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Best Local Similarity 33...
Best A; Conservative
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                                        Best Local Similarity 33.3
Matches 4; Conservative
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                                                                                                                                              56 RRPSSATARSSR 67
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Best Local Similarity
Matches 4; Conserv
                         Query Match
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RESULT 13

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Sequence 33676, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 00/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield and MINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
FILE REFERENCE: 107196.136
CURRENT PILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24681
LENGTH: 139
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Pred. No. 6e+02;
0; Mismatches 8; Indels
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Pred. No. 6e+02;
0; Mismatches (
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Similarity 33.3%;
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Matches 4; Conservative
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210, App 210, App 210, App 37, Appl 32306, A 147658, 350524, 338158, 173763,

Sequence Sequence Sequence

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Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

Result

Sequence 3 Sequence 3 Sequence 1

8, Appli 3, Appli

Sequence Sequence

Appli

46297, P 72973, P 50703, P 168937, 125004,

Sequence 194527

Sequence Sequence Sequence

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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 124, Application US/10085198

Sequence 124, Application US/10085198

Bublication No. US20040009907A1

GENERAL INFORMATION:
APPLICANT: Albobrook et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-279

CURRENT APPLICATION NUMBER: US/10/085,198

CURRENT PILING DATE: 2002-02-25

PRIOR PELING DATE: 2001-02-26

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-08-13
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US-10-425-114-59856
                                                      US-10-282-122A-50703
US-10-437-962-12504
US-10-084-846A-8
US-10-084-846A-3
US-10-084-846A-3
US-10-094-210
US-10-7050-704-210
US-10-7050-701-55011
US-10-029-386-32306
US-10-0437-963-147658
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33.3%; Pred. No. 2.2e+03;
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US-10-425-115-338158
US-10-424-599-173763
          US-10-437-963-150101
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US-10-425-114-72973
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; Sequence 59856, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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Best Local Similarity 33.3
Matches 4; Conservative
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19608
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US-10-085-198-124
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Sequence 4, Appli
Sequence 5, Appli
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Sequence 45211, A
Sequence 18403,
Sequence 10480,
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118401,
50352, A
48089, A
113409,
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194450,
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3948, Ap
67642, A
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Sequence 124, App
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                                                                                                                 March 29, 2006, 02:05:02 ; Search time 119 Seconds (without alignments) 49.156 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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/: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-085-198-124
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US-09-905-691-5
US-09-905-691-2
US-10-425-114-45271
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US-10-425-114-328436
US-10-425-115-325436
US-10-425-115-325436
US-10-425-115-325436
US-10-425-114-8080
US-10-092-154-886
US-10-092-154-886
US-10-092-154-886
US-10-425-114-48089
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                                                                                                                                                                                                                                                                                                  1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2. US-10-084-846A-4
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APPLICANT: Wolz, Kussell L.
APPLICANT: Wolz, Gabriella
TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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95.0%; Score 19; DB 4; Length 197
Best Local Similarity 33.3%; Pred. No. 6.1e+04;
Matches 4; Conservative 0; Mismatches 8; Indels
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                            APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREEZER, AXEL
APPLICANT: TREEZER, AXEL
TITLE OF INVENTION: AUTHANYCIN DERIVATIVES
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REPRENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EPO1/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 4
SEC ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Tris-Arginine Helix #3
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09905691; Publication No. US20020164329A1; GENERAL INFORMATION:
        APPLICANT: WEITNAUER, GABRIELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11142 RRRSSTASRTSR 11153
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Sequence 162715, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zoo, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT SEQ ID NOS: 204966

SEQ ID NO 162715

LENTH: 712
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PRIOR APPLICATION NUMBER: 60/312,858
PRIOR FILING DATE: 2001-08-16
PRIOR PLING DATE: 2001-08-16
PRIOR PLING DATE: 2001-02-27
PRIOR PLING DATE: 2001-02-27
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2001-04-21
PRIOR PLING DATE: 2001-04-21
PRIOR PLING DATE: 2001-06-20
PRIOR PLING DATE: 2001-08-29
PRIOR PLING DATE: 2001-02-24
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US-10-437-963-162715
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-437-963-162715
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US-10-084-846A-4
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| Sequence 2, Application US/09905691
| Publication No. US20020164329A1
| GENERAL INFORMATION:
| APPLICANT: Harris, Robert B.
| APPLICANT: Wolz, Gabriella
| TITLE OF INVENTION: Adeorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Adeorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Huide Using Cationic Helix Peptides
| TITLE OF INVENTION: UNMERR: US/09/905,691
| CURRENT APPLICATION NUMBER: US/09/905,691
| CURRENT FILING DATE: 2001-02-14
| NUMBER OF SEQ ID NOS: 5
| SEQ ID NO 2
| SEQ ID NO 2
| LENGTH: 19
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Son, Yongwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION WUMBER: US/10/425,114
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Pred. No. 4.1e+02;
0; Mismatches 8; Indels
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TITLE OF INVENTION: Fluids Using Cationic Helix Peptides FILE REFERENCE: 006338-017
CURRENT APPLICATION NUMBER: US/09/905,691
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 5
SECTION SECURE FARESEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 16
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Bis-Arginine Helix #2
US-09-905-691-2
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; Sequence 45271, Application US/10425114
; Publication No. US20040034888A1
; GRNERAL INFORMATION:
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Matches 4; Conserva
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Sequence 184083
; Sequence 184083
; Sequence 184083 Application US/10437963
; Publication No. US2004012334341
; Publication No. US2004012334341
; Publication No. US2004012334341
; Publication No. US2004012334341
; APPLICANT: La Rosa, Thomas J.
    APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184083
; LENGTH: 87
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j Sequence 325436, Application US/10425115
j Publication No. US20040214272A1
j Publication No. US20040214272A1
j APPLICANT: La Rosa, Thomas J.
j APPLICANT: Zhou, Yihua
j APPLICANT: Zhou, Yihua
j APPLICANT: Cao, Yongwei
j TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
j TITLE OF INVENTION: Plants
j TITLE OF INVENTION NUMBER: US/10/425,115
j CURRENT FILING DATE: 2003-04-28
j NUMBER OF SEQ ID NOS: 369326
j SEQ ID NO 325436
j LENGTH: 118
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Pred. No. 1.4e+03;
0; Mismatches 8; Indels
                                                                                                                                 Length 64;
                                                                                                                                 Score 18; DB 4; Length 64;
Pred. No. 1.1e+03;
0; Mismatches 8; Indels
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US-10-437-963-184083
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                                                                , OTHER INFORMATION: Clone ID: 700431372_FLI.pep
US-10-425-114-45271
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33.3%;
                                                                                                                                 Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity 33.3.
Local 4; Conservative
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ORGANISM: Zea mays
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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Gaps

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NAME/KEY: SITE
LOCATION: (94)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-847-886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (85)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 886, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 2003

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 886

LENGTH: 127
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                                                                                                               Score 18; DB 4; Length 124; Pred. No. 1.9e+03; 0; Mismatches 8; Indels
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; Publication No. US20030054375A1
; GRNERAL INFORNATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
                      ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24656C.1.pep
US-10-425-115-286800
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                 Query Match 90.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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NAME/KEY: SITE
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US-10-092-154-886
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104880
LENGTH: 120
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; Sequence 286800. Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Stou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REPERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286600
; LENGTH: 124
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Pred. No. 1.8e+03;
0; Mismatches 8; Indels
                                              Length 118;
                                         Score 18; DB 4; Length 118
Pred. No. 1.8e+03;
0; Mismatches 8; Indels
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US-10-437-963-104880
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LOCATION: (1)..(120)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
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33.3%;
                      Query Match
Best Local Similarity 33.3.
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Best Local Similarity 33.3
Matches 4; Conservative
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ORGANISM: Oryza sativa
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NAME/KEY: unsure
LOCATION: (1)..(124)
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ORGANISM: Zea mays
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US-10-425-115-325436
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APPLICANT: LA KOVALICANT
APPLICANT: LA KOVALICANT
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 118401
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (85)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc feature
LOCATION: (111)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-886
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Pred. No. 1.9e+03;
0; Mismatches 8; Indels
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US-10-437-963-118401
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SEO FWARE: Patentin Ver. 2.0
SEO ID NO 886
LENGTH: 127
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LOCATION: (1)..(134)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 33.3%;
Matches 4; Conservative
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                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                           NAME/KEY: misc feature
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90.0%; Score 18; DB 4; Length 134;

Query Match

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      Best Local Similarity 33.3%; Pred. No. 2e+03;

      Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps

      Qy 3 RRXXXXXRXRXR 14

      Db 81 RRRATATRARA 92

      Search completed: March 29, 2006, 02:10:40

      Job time: 120 secs
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ORGANISM: Glycine max
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US-11-096-568A-25321
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34, Appl
10728, Appl
10728, A
10930, A
16604, Ap
6884, Ap
6884, Ap
556, App
22603, A
22434, Ap
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Appli
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16, Appl
25670, A
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Sequence 25321, A
Sequence 27148, A
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                                                                                                               March 29, 2006, 02:06:17 ; Search time 13.125 Seconds (without alignments) 31.461 Million cell updates/sec
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| SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*
| SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*
                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-096-568A-2531

US-11-096-568A-27148

US-11-078-469-71

US-11-078-469-71

US-11-078-469-71

US-11-078-469-71

US-11-078-468-71

US-11-096-568A-19930

US-11-096-568A-20087

US-11-096-568A-2604

US-11-096-568A-22603

US-11-096-568A-22603

US-11-096-568A-22603

US-11-096-568A-24037

US-11-096-568A-24037

US-11-096-568A-2404

US-11-096-568A-2404

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US-11-096-568A-2404

US-11-124-367A-466

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US-11-096-568A-25670
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                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    174695 segs, 29494374 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Perfect score:
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26 16 80.0 104 7 US-11-096-568A-13882 Sequence 13882, A 27 16 80.0 105 7 US-11-096-568A-7047 Sequence 7047, Ap 28 16 80.0 160 160 7 US-11-096-568A-1539 Sequence 14539, A 29 16 80.0 160 160 7 US-11-096-568A-12510 Sequence 14510, A 29 16 80.0 167 7 US-11-096-568A-12510 Sequence 25510, A 31 16 80.0 167 7 US-11-096-568A-25509 Sequence 25510, A 21 16 80.0 174 7 US-11-096-568A-26671 Sequence 26671, A 21 16 80.0 174 7 US-11-096-568A-26671 Sequence 26671, A 21 16 80.0 174 7 US-11-096-568A-26671 Sequence 18247, A 21 16 80.0 186 7 US-11-096-568A-26671 Sequence 1230, Ap 24 16 80.0 189 7 US-11-096-568A-18247 Sequence 1230, Ap 24 16 80.0 189 7 US-11-096-568A-18246 Sequence 1676, Ap 24 16 80.0 193 7 US-11-096-568A-18246 Sequence 1676, Ap 24 16 80.0 194 7 US-11-096-568A-18256 Sequence 1676, Ap 24 16 80.0 206 7 US-11-096-568A-18256 Sequence 24216, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 24216, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18556, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18556, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18556, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18556, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18596, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 18596, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 24216, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 1599, Ap 24 16 80.0 206 7 US-11-096-568A-2429 Sequence 1599, Ap 250 7 US-11-096-568A-24216 Sequence 1599, Ap 250 7 US-11
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ALIGNMENTS

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WESULT 1

US-11.096-568A-4518

US-11.096-568A-4518

Sequence 4518, Application US/11096568A

Sequence 4518, Application No. US2006004840A1

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVERTION: Thereby.

TITLE OF INVERTION: Thereby.

TITLE OF INVERTION: Thereby.

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

NUMBER OF SEQ ID NO 4518

LENGTH: 141

ORDANISH: Glycine max

NAME/KEY: misc_feature

LOCATION: (1)-(141)

OGNET NIFRORMATION: Ceres Seq. ID NO. 13638657

US-11-096-568A-4518

OGNET NEROMATION: (1)-(141)

Matches 4; CONSETVATION: OF Mismatches 8; Indels 0; Gaps 0;

RESULT 2

NAME/KEY: Machine No. US/20060048340A1

Sequence 25321, Application US/1108658A

PRESULT 2

Sequence 25321, Application US/1108658A

PRESULT 2

Sequence 25321, Application US/1109658A

PRESULT 2

SEQ ID NO. 25321

SEQUENCE 25321, Application US/1109658A

CURRENT PROPARATION: Sequence Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVERTION: Thereby

TITLE OF INV
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APPLICANT: HART, SCOTT A.
APPLICANT: EEH, KARIN
APPLICANT: ECH, KARIN
APPLICANT: STOLOW, DAVID
APPLICANT: STOLOW, DAVID
APPLICANT: CONGER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT PILLING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR PLILOR DATE: 2004-03-18
PRIOR PLILOR DATE: 2004-015-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HART, SCOTT A.
APPLICANT: EZH, KARIN
APPLICANT: EZH, KARIN
APPLICANT: ZCH, CARIN
APPLICANT: CONGER, DE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR FILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Ver. 3.3
: SEG ID NO 71
LENGTH: 32
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide moiety
FEATURE:
NAME/KEY: MOD_RES
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Pred. No. 56;
0; Mismatches 8; Indels
                                                                                                                                                Sequence 34, Application US/11078469
Publication No. US20050282755A1
GENERAL INFORMATION:
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Publication No. US20050282755A1
GENERAL INFORMATION:
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illarity 33.3%;
Conservative c
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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Sublication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBORE: 2790-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27148
LENGTH: 341
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Sequence 33, Application US/11182016

Publication No. US20060019294A1

GENERAL INFORMATION:

APPLICANT: SUGEN, INC.

TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS

FILE REFERENCE: 038602/0102

CURRENT APPLICATION NUMBER: US/11/182,016

CURRENT FILING DATE: 2005-07-15

PRIOR APPLICATION NUMBER: US/09/958,359

PRIOR PILING DATE: 2002-02-05

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 496
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US-11-182-016-33
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                                                                                                                                                      Score 18; DB 7; Length 101;
Pred. No. 78;
0; Mismatches 8; Indels
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NAME/KEY: misc feature
COCTION: (1): (341)
OTHER INFORMATION: Ceres Seq. ID no. 15175533
US-11-096-568A-27148
                                   ; LOCATION: (1)...(101)
; OTHER INFORMATION: Ceres Seq. ID no. 13580080
US-11-096-568A-25321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                    3 RRXXXXXXXX 14
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NAME/KEY: misc_feature
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OP INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO FRO ID NOS: 34471
SEQ ID NO 16604
LENGTH: 200
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; Publication No. US20060041961A1
; GENERAL INFORMATION:
GABLERAL TABLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%; Score 17; DB 7; Le 33.3%; Pred. No. 2.7e+02; ive 0; Mismatches 8;
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Pred. No. 2.6e+02;
0; Mismatches 8
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LOCATION: (1)...(192)

CTHER INFORMATION: Ceres Seq. ID no. 12375688

US-11-096-568A-19930
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| LOCATION: (1)...(200)
| OTHER INFORMATION: Ceres Seq. ID no. 12353107
| US-11-096-5688-16604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16604, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Best Local Similarity 33...
Best Local Similarity
4, Conservative
Best Local Similarity 33.3
Matches 4; Conservative
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                   셤
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 189
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                                                                                                                                                                                                                                                                                                           US-11-087-099-10728

Sequence 10728, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

TITLE OF INVENTION: Genes and Uses for Plant Improvement;

TITLE OF INVENTION: Genes and Uses for Plant Improvement;

CURRENT APPLICATION UNDMER: US/11/087,099;

CURRENT PILING DATE: 2005-03-22;

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 10728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.0%; Score 17; DB 7; Length 173; Best Local Similarity 33.3%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 8; Indels
                                                                                                                              DB 7; Length 32;
56;
                                                                                                                                                                  8; Indels
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: LOCATION: (1)...(173)

: CHER INFORMATION: unsure at all Xaa locations

US-11-099-10728
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i LOCATION: (1)..(189)
corner incomation: Ceres Seq. ID no. 12376847
US-11-096-568A-20087
                                                                                                                                                                    0; Mismatches
                                                                                                                                Score 17;
Pred. No.
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   OTHER INFORMATION: peptide moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays subsp. mays
                                                                                                                              h 85.0%;
Similarity 33.3%;
4; Conservative (
                                      NAME/KEY: MOD_RES

| LOCATION: (1)

| OTHER INPORMATION: H2N-Arg

US-11-078-469-71
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Best Local Similarity
Matches 4, Conserva
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Publication No. US20060048240A1

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICATOR:

TITLE OF INVENTION:

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TITLE OF INVE
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Publication No. US2006048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1992P29, 11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

EENGTH: 277
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         Score 17; DB 6; Length 274;
Pred. No. 3.5e+02;
0; Mismatches 8; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 12375687
US-11-096-568A-19929
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; LOCATION: (1)...(274)
; OTHER INFORMATION: Ceres Seq. ID no. 12409336
US-11-096-5688-22603
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      Similarity 33.3%;
4; Conservative
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Best Local Similarity 33.3
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ORGANISM: Zea mays subsp.
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NAME/KEY: misc_feature
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US-11-096-568A-19929
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US-11-096-568A-20086
US-11-096-568A-20086
US-11-096-568A-20086
Sublication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Tharby
TITLE OF INVENTION: Tharby
TITLE OF INVENTION: 1592-1692-1692
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PELICATION NUMBER: US/11/096,568A
MUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20086
LENGTH: 212
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Sequence 956, Application US/10821234

Publication No. US20050255114A1

Sequence 956, Application US/10821234

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PLSC_Genes Version 1.0

SEQ ID NO 956

LENGTH: 274
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Pred. No. 2.8e+02;
0; Mismatches 8; Indels
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; LOCATION: (1)...(212)
; OTHER INFORMATION: Ceres Seq. ID no. 12376846
US-11-096-5688-20086
      FILE REFERENCE: 38-21(51450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6884
LENGTH: 211
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Best Local Similarity 33.3.3
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Best Local Similarity 33.3.
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; ORGANISM: Homo sapiens
US-10-821-234-956
                                                                                                                                                                                                                           ; ORGANISM: Zea mays
US-11-087-099-6884
                                                                                                                                                                                                     TYPE: PRT
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March 29, 2006, 01:38:52; Search time 159.75 Seconds (without alignments) 49.507 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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geneseqp2000s:*
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Maximum DB seq length: 200000000
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98
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ado34231 Synthetic Ado34225 Synthetic Ado34228 Synthetic Ado34239 Synthetic Ado34231 Synthetic Ado34318 Synthetic Ado34318 Synthetic Ado34318 Synthetic Ado34319 Synthetic Ado34240 Synthetic Ado34247 Synthetic Ado34247 Synthetic Ado34227 Synthetic Ado34227 Synthetic Ado34318 Synthetic Ado34348 Synthetic Ado34240 Synthetic	
SUMMARIES	AD034231 AD034228 AD034228 AD034236 AD034334 AD034354 AD034350 AD034237 AD034276 AD034227 AD034220 AD034244 AD034244 AD034244 AD034241 AD034241	20252000
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8 8 ADO34239 8 8 ADO34344 8 8 ADO34215 8 8 ADO34245		60 00 00		
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25 26 27 28		33 35 36 36	38 38 4 39 4 0	4 4 4 4 1 4 4 4 4 1 5 6 4 6

ALIGNMENTS

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL. Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8. Datta G; Apo34231 standard, peptide, 18 AA. Anantharamiah GM, Garber DW, 13-NOV-2002; 2002US-0425821P. 13-NOV-2003; 2003WO-US036268 12-AUG-2004 (first entry) (UABR-) UAB RES FOUND WPI; 2004-411629/38. WO2004043403-A2. 27-MAY-2004. Synthetic. AD034231; RESULT 1

AD034231

ID AD034231

XXX AD034231

XXX AD07

BY AD07

Claim 4; SEQ ID NO 8; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E

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cardiant, vasotropic, antiarterioscierotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysberalipoproteinaemia or atheroscalerosis; and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; VLDL.
mimicking polypeptide has the following activities: antilipaemic,
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                                                                                                                                                                                                                                                                                                           100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO34225 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                             Anantharamiah GM, Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2003; 2003WO-US036268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004043403-A2
                                                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD034225;
                                                                                                                                                                                                                                                                                                             Query Match
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CC (including animal or plant) comprising the synthetic apolipoprotein-E minicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E minicking polypeptide and a carrier; and an ennoclonal antibody that specifically binds to the synthetic apolipoprotein-E minicking polypeptide. The synthetic apolipoprotein-E minicking polypeptide has the following activities: antilipsemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is cardiant, vasotropic, antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, companzee or orangutan); for treating coronary artery disease, companze or orangutan); for treating coronary artery disease, companze or orangutan); for treating coronary artery disease, companze or orangutan); for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (ULDL) or very low coult, by a cell. This sequence represents a synthetic apolipoprotein-E minicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; DB 8; Length 18; Pred. No. 6.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 5; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GIRRFLGSIWRFIRAFYG 18
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Beet Local Similarity 100...
Beet Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein E minicking polypeptide is antianginal. The synthetic apolipoprotein E minicking polypeptide is useful for reducing serum cholescerol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, myocardial infarction or atheroscleroslis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E minicking density lipoprotein (VLDL) to a cell and enhances degradation of EDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein.
mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mimicking polypeptide of the invention.
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100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.1e-08; Mismatches ö 18 1 GIRRFLGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18; Conservative Similarity Query Match Best Local 9 Matches ઠે g

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13. ADO34236 standard; peptide; 18 AA. (first entry) 12-AUG-2004 AD034236; RESULT 4 AD03423

apolipoprotein-E mimicking polypeptide, antilipaemic, cardiant; vasotropic, antiarteriosclerotic, cerebroprotective, antianginal; serum cholesterol, coronary artery disease; dysbetalipoproteinaemia, atherosclerosis; myocardial infarction; stroke, embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; ULDL.

Synthetic

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Synthetic apolipoprotein-E mimicking polypeptide useful for treatir coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. ö Datta Anantharamiah GM, Garber DW, WPI; 2004-411629/38.

Claim 4; SEQ ID NO 13; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or atransgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising

the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic.

CC mimicking polypeptide has the following activities: antilipaemic.

CC ardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is cuseful for reducing serum cholesterol in a subject (including a mammal cuseful for reducing serum cholesterol in a subject (including a mammal cuch mapanzee or orangutan); for treating coronary artery disease,

CC dybbetalipoproteinamenia or atherosclerosis; and for reducing the risk of mycardial infarction or stroke; for breaking and for reducing the subject;

CC and also for treating angina. The synthetic apolipoprotein-E mimicking chapted enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) or very constitution polypeptide of the invention. Sequence 18 AA;

Gaps ö Length 18; Indela 100.0%; Score 98; DB 8; I 100.0%; Pred. No. 6.1e-08; Mismatches ö 18; Conservative Query Match Best Local Similarity Matches 18; Conserv

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1 GIRRFLGSIWRFIRAFYG 18

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Gaps

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0; Indels

ADO34233 standard; peptide; 18 AA ADO34233; RESULT 5 ADO34233

12-AUG-2004 (first entry)

Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 10.

apolipoprotein-B mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina, low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW, Datta

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 10; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host call, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

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c an monoclonal antibody that specifically binds to the synthetic

c apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

c mimicking polypeptide has the following activities: antilippementc,

c ardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

c antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

cusful for reducing serum cholesterol in a subject (including a mammal

c such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

c chimpanzee or orangutan); for treating coronary artery disease,

cc dyabetalipoproteinaemia or atherosclerosis; and for reducing the risk of

myocardial infarction or stroke; for breaking an embolus in the subject;

and also for treating angina. The synthetic apolipoprotein-E mimicking

polypeptide enhances binding of low-density lipoprotein (LDL) or very low

density lipoprotein (VLDL) to a cell and enhances degradation of LDL or

VLDL by a cell. This sequence represents a synthetic apolipoprotein-E

mimicking polypeptide of the invention.
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Sequence 18 AA;

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Gaps
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  100.0%; Score 98; DB 8; Length 18;
                       0; Indels
            Pred. No. 6.1e-08;
                         Mismatches
                         .;
0
                                                1 GIRRFLGSIWRFIRAFYG 18
                                                              GIRRELGSIWRFIRAFYG 18
               100.08;
                         18; Conservative
Query Match
Best Local Similarity
                          Matches
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ADO34314 standard; peptide; 18 AA AD03431

(first entry) 12-AUG-2004 AD034314;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;

Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

ö Datta Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid aencoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypudleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 131; 79pp; English.

Datta G;

Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

(UABR-) UAB RES FOUND.

13-NOV-2003; 2003WO-US036268 13-NOV-2002; 2002US-0425821P

WO2004043403-A2.

Synthetic

27-MAY-2004

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiarteriosclerotic, cerebroprotective, and cartianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating ocronary artery disease, and subject in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking chospetide enhances binding of low-density lipoprotein. E mimicking changing of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131.
                                                                                                                                                                                                                                                                    Score 95; DB 8; Length 18;
Pred. No. 1.8e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                           Sequence 18 AA;
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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiangular, vasotropic, antiarteriosclerotic, cerebroprotective, and antiangulal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or a therosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention. mimicking polypeptide has the following activities: antilipaemic, 8X8888888888888X8

Sequence 18 AA;

Gaps ö Score 94; DB 8; Length 18; Pred. No. 2.5e-07; 2; Mismatches 0; Indels 5 1 GIRRFLGSIWRFIRAFYG 18 95.9%; Local Similarity 88.9 Query Match ઠે g

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ADO34338 standard; peptide; 18 (first entry) 12-AUG-2004 AD034338; RESULT 8 AD034338

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol, coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

UABR-) UAB RES FOUND

Datta Anantharamiah GM, Garber DW,

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WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 115; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide are composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,

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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or a therosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein-E mimicking density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vāsotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.
                                                                                                                                                                                                                                                                                                        95.9%; Score 94; DB 8; Length 18;
88.9%; Pred. No. 2.5e-07;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLRRFIGSIWRFIRAFYG
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                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD034352;
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useful for reducing serum cholesterol in a subject (including a mammal

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. Emminicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities; antilipaemic, cardiant, vasotropic, antiateriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.
                                                                                                                                                                                                                                                                                           Score 94; DB 8; Length 18;
Pred. No. 2.5e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO34340 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                         95.9%;
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                                                                                                                                                                                                                                                                                                                                  16; Conservative
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                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                      Sequence 18 AA;
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Best Local 9
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ID ADO3
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        such as a mouse, rat, rabbit cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, and systetalipoproteinsemia or atheroscelerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymocleotide; a composition comprising an monoclonal antiboprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosclerotic, carebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
                                                                                                                                                                                                                                                                  Score 94; DB 8; Length 18;
Pred. No. 2.5e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      95.9%;
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nes 16; Conservative
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                                                                                                                                                                                                                                Sequence 18 AA;
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Matches
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chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention. sheep, pig, human, monkey, ape, COW, rat, rabbit, such 8888888888888

Sequence 18 AA;

Gaps ö Score 94; DB 8; Length 18; Pred. No. 2.5e-07; 2; Mismatches 0; Indels 5 1 GIRRFLGSIWRFIRAFYG 18 18 95.9**%**; 88.9**%**; 1 GLRRFIGSIWRFIRAFYG Best Local Similarity 88.9 Matches 16; Conservative Query Match g ઠે

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ADO34297 standard; peptide; 18 AA. ADO34297

(first entry) 12-AUG-2004

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestreol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; ULDL.

Synthetic

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 74; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide ancoding polymucleotide; a composition comprising an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, on-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymedicetide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal micking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabblt, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 21; 79pp; English.

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Garber DW,

WPI; 2004-411629/38. Anantharamiah GM,

(UABR-) UAB RES FOUND

13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P

WO2004043403-A2

27-MAY-2004

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chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of mycoardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
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                                                                                                                                            93.9%; Score 92; DB 8; 1
88.9%; Pred. No. 5.1e-07;
                                                                                                                                                                       Mismatches
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Best Local Similarity 88.3.
Best Local Similarity
Local Similarity
Local Similarity
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                                                                                                                       Sequence 18 AA;
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for reducing serum cholesterol in a subject (including a mammal

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dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypetide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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/note= "All Lys residues are DiMethyl-Lysine"
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88.9%; Pred. No. 5.1e-07
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16; Conservative
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                                                                                                                                                                      Sequence 18 AA;
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Modified-site
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      such as a mouse, rat, rabbit cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, adysbetalipoproteinaemia or atheroscelerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                           Score 92; DB 8; Length 18;
Pred. No. 5.1e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO34227 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                                93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2003; 2003WO-US036268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-2002; 2002US-0425821P
                                                                                                                                                                                                                                                                                                                                             1 GIRRELGSIWRFIRAFYG
                                                                                                                                                                                                                                                                                                                                                                  1 GIKRFLGSIWRFIKAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                   Local Similarity 88.9
es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-411629/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004043403-A2.
                                                                                                                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD034227;
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO34227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8888888888888888
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such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention. 88888888888888

Sequence 18 AA;

Gaps ; Query Match 91.8%; Score 90; DB 8; Length 18; Best Local Similarity 94.4%; Pred. No. 1e-06; Matches 17; Conservative 0; Mismatches 1; Indels

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ઠ g Search completed: March 29, 2006, 01:44:08 Job time : 159.75 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 29, 2006, 01:44:43 ; Search time 26.4375 Seconds (without alignments) 65.509 Million cell updates/sec

US-10-712-447-5 98 1 GIRRFLGSIWRFIRAFYG 18 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 80:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	transcription regu	2-oxoglutarate/mal	poly (3-hydroxybuty	leucyl-tRNA synthe	leucine-tRNA ligas	acriflavin resista	hypothetical prote	0		NIP1 protein - yea	TMV resistance pro	reverse transcript	penicillin-binding	c			hypothetical prote	9		ä	н	MHC class I histoc	HLA-A-0	class I	class I	class I hi	MHC HLA-A2.4a chai	gene HLA-A-0205 pr
	DI	S76462	A75578	G64537	A34341	A84060	H64102	AH3568	T32316	B84733	T33269	A46417	T04583	T12085	E84953	T52113	D72540	T15530	B72692	154412	F71707	D97700	HLHU69	HLHUA2	138443	161902	137542	I84448	161857	138442
	DB	2	~	Н	~	~	~	~	~	~	~	N	~	7	7	~	~	~	~	~	~	N	-	-	~	~	~	~	~	7
	Length	627	178	461	589	806	861	1025	265	489	516	812	1607	407	760	107	214	228	237	246	258	258	273	365	365	365	365	365	365	365
, i	Match	49.0	45.9	44.9	44.9	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	43.4	43.4	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	٠.	42.9	42.9	42.9	•
	Score	48	45	44	44	44	44	43.5	43	43	43	43	43	42.5	42.5	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
1,000	No.	-	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	leucyl-tRNA synthe	leucyl-tRNA synthe		leucine-tRNA ligas	homolog to drosoph	hypothetical prote	rfaP protein - Esc	dimethylgulfoxide	hypothetical prote	hypothetical prote	probable permease	hypothetical prote	hypothetical prote	hypothetical prote	cytochrome P450 DW
T04745	AD1282	AH1653	B89961	D69650	T50337	AG2115	C42595	E64109	T20575	AF2599	G97381	T08940	F96571	D96776	T02263
7	N	~	~	~	7	~	~	7	~	~	~	0	~	~	-
537	803	803	804	804	790	131	265	279	359	364	364	384	406	503	519
42.9	42.9	42.9	42.9	42.9	42.3	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
42	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

576462	
hypothetical protein - Synechocystis sp. (strain PCC 6803)	6803)
C;Species: Synechocystis sp.	
A;Variety: PCC 6803	
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004	ext_change 09-Jul-2004
C; Accession: S76462	
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;	lzu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda	r.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996	
A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis	ellular cyanobacterium Synechocystis
A;Reference number: S74322; MUID:97061201; PMID:8905231	231
A;Accession: S76462	
A;Status: preliminary	
A; Molecule type: DNA	
A;Residues: 1-627 <kan></kan>	
A,Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID	C103F; EMBL: D90915; GB: AB001339; NID
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996	EMBL Data Library, June 1996
Onerv Match 49.0%; Score 48; DB 2; Length 627;	Length 627;
Best Local Similarity 38.9%; Pred. No. 8.1;	
Matches 7. Conservative 6. Mismatches 5. Indels 0: Gads	Indels 0; Gaps 0;

|: || ||::| || || 597 GLEQLLGKIWQWLRQKFG 614 1 GIRRFLGSIWRFIRAFYG 18 ઠે

7; Conservative Matches

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transcription regulator, MarR family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75578
R;Milte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S; Smitch, H.O.; Venter, J.C.; Praser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Accession: A75578
A;Accession: A75578
A;Accession: A75578
A;Accession: A7578
A;Accession: A7578
A;Accession: A7578
A;Accession: A7578
A;Accession: BNA
A;Residues: 1-178 cWHI>
A;Accessives: UNIPROT:Q9RYRO; UNIPARC:UPIO000D3BE4; GB:AE001863; GB:AE001825; NIF

C,Genetics: A,Gene: DRA0248

45.9%; Score 45; DB 2; Length 178; Query Match

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CjAccession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç A;Reference number: A83650, MUID:20512582; PMID:11058132
A;Accession: A84060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:g15'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:09K7S8; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cjaccesion: H64102
RjFleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayno, S.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. D.M.; Brandon, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Puhrmann, J.L.; Geoghagen, N.S.M.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Puhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Ajathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                    leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-861 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 861;
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46.2%; Pred. No. 48;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 53.8%; Pred. No. 45;
hes 7; Conservative 2; Mismatches 4
100 RRFAGDAWRTNLPYRFAAAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: leuS
C,Superfamily: leucine-tRNA ligase
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GAKRFLGRVWNLV 677
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GARRFLDRVWRLL 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: H64102
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Matches
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RiTomb, J.F.; Whalte, O.; Kerlaavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, J.F.; Whalte, O.; Kerlaavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64537
A;Accession: G64537
A;Residues: prediminary; nucleic acid sequence not shown; translation not shown
A;Mesidues: 1-461 crows
A;Residues: 1-461 crows
C;Superfamily: 2-oxoglutarate/malate translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A3431

poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species Alcaligenes eutrophus
C;Species 12-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J.
B;Peoples, O.P.; Sinskey, A.J.
A;Title: Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Iden
A;Reference number: A34341; MUID:89359357; PMID:2670936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A39190
A;Status: preliminary
A;Nolecule type: DNA
A;Reaidues: 1-219 <SCH>
A;Reaidues: 1-219 <SCH>
A;COSS-references: UNIPARC:UPI000016E162; GB:M64341; NID:G141864; PIDN:AAA21979.1; PID:
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:G141864; PIDN:AAA21979.1; PID:
C;Superfemily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT: P23608; UNIPARC: UPI0000044953; GB:J05003; NID:g141958; PIDN:
A;Cross-references: Exrain H16
R;Schubert, P;Krueger, N; Steinbuechel, A.
J; Bacteriol. 173, 168-175, 1991
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                                     ö
                                                                                                                                                                                                                                                                                                                                                                  C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                     Gaps
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                                                                                                                                                                                                                                                                                                                                    2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 461;
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                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A39190; MUID:91100279; PMID:1987116
                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1;
Pred. No. 26;
2; Mismatches 4
                                     Mismatches
      Pred. No.
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   69.2%;
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297 VRRLLSWFWRFVR 309
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   Best Local Similarity 69.2
Matches 9, Conservative
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Best Local Similarity
Matches 10; Conserv
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NIPI protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protein NyAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protein Species: Saccharomyces cerevisiae
C;Species: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S53302
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIPI, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
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A;Reaiduea: 571-582,'Q',584-640,'K',642,'K',644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:g798940; PID:g798951; MIPS:Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-110,'V','112-582,'Q',584-602 <CHU>
A;Cross-references: UNIPARC:UP10000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:076442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.
A;Experimental source: strain Bristol N2; clone C2489
A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C24B9.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
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A;Reaidues: 1-812 <GU1>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849; NCBIP:117850)
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A;Description: The sequence of C. elegans cosmid C24B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
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42;
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ubunitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
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A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
                                                                                                               Score 43; DB 2
Pred. No. 40;
4; Mismatches
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submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
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43.9%; Score 43;
Best Local Similarity 41.2%; Pred. No. 4
Matches 7; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IRRFLGSIWRFIRAFYG 18
                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                               6 LGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                           :|::| |:||
54 IGNMWSFLRAF 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: 73316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F31F4.
A;Reference number: 221149
A;Accession: T32316
A;Accession: T32316
A;Accession: T32316
A;Residues: 1-265 <BLA>
A;Residues: 1-265 <BLA>
A;Residues: 1-265 <BLA>
A;Residues: 1-265 <BLA>
A;CGGESTERSER BONA
A;Residues: 1-265 <BLA>
A;CGGESTERSER BONA
       Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A,Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A,Reference number: AD3252; PMID:11756688
A,Reference LAH356B
A,Residue: AH356B
A,Residue: PROJS - KUR>
A,Residues: 1-1025 - KUR>
A,Residues: 1-1025 - KUR>
A,Residues: 1-1025 - KUR>
A,Cross-references: UNIPROT:08YCO5; UNIPARC:UPI0000584C8; GB:AE008918; PIDN:AAL53715.1;
A,Experimental source: strain 16M
C,Genetics:
A,Gene: BMEI10473
A,Map position: II
C,Superfamily: hypothetical protein b2075
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Mcarman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Coss-references: UNIPROT:092V72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 44.4%; Score 43.5; DB 2; Length 1025; Similarity 50.0%; Pred. No. 69; 8; Conservative 4; Mismatches 1; Indels 3;
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Pred. No. 22;
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531 FLGSVWSFMTLPRSFF 546
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Af A;Reference number: A84930; MUID:20445173; PMID:10993077
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A;Cross-references: UNIPROT:065154; UNIPARC:UPI00000C45F; EMBL:AF053302; PIDN:AAC08574.1
A;Experimental source: cultivar Columbia
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C, Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Status: preliminary
A; Molecule 1.796: DNA
A; Residues: 1-760 <STO>
A; Cross-references: UNIPARC:UP1000005E4C8; GB:AP000398; GSPDB:GN00144
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R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E.
R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E.
Plant J. 14, 685-92, 198
A;Title: Isolation of putative plant transcriptional cost A;Reference number: Z25848; MUID:98346011; PMID:9681033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; |
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: penicillin-binding protein 1B
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Job time : 28.4375 secs
||| ||| : |||| |
178 GIRSFLGHVGFYRRFIRDF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 INRFINGKVWNFPTSIYG 49
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54 VRNWNGKIWIDIREFY 69
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Local Similarity 44.4%;
les 8; Conservative
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Best Local Similarity 50.0°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: mrcB; BU200
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Matches
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T04583
TWV resistance protein N homolog F23E13.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: 104583; T05507
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T. submitted to the Protein Sequence Database, March 1998
A;Reference number: 215378
A;Accession: T04583
A;Molacule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT:O65506; UNIPARC:UPIO0000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
B;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
A;Reference number: 215418
A;Accession: T05507
A;Accession: T05507
A;Accession: T469-1607 <BE2>
A;Cross-references: UNIPARC:UPIO0016DBFD; EMBL:AL022373
A;Cross-references: UNIPARC:UPID00016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reverse transcriptase homolog - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
Submitted to the EMBL Data Library, September 1997
A;Rescription: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: Z17406
A;Reference number: Z17406
A;Reference number: Z17406
A;Ression: T12085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.9%; Score 43; DB 2; Length 1607; 72.7%; Pred. No. 1.3e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                              Length 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270
                                                                                                                                                                                       Score 43; DB 2;
Pred. No. 66;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.4%; Score 42.5; D
57.9%; Pred. No. 40;
tive 1; Mismatches
               C;Genetics:
A;Gene: SGD:NIP1
Z;Cross-references: SGD:S0004926; MIPS:YMR309c
A;Map position: 13R
                                                                                                                                                                                       Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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361 GVKRILGSIFSFV 373
                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFI 13
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity
Matches 11; Conserva
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Gaps

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Gaps

1 GIRRFLGSIW---RFIRAF 16

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Title: US-10-712-447-5
Perfect score: 98
Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Sequence: 1 GIRRFLGSIWRFIRAFYG 18 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 216

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Uniprot 05.80:* 1: uniprot sprot:* 2: uniprot_trembl:* bred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q25271 leptinotars		Q4lk44 burkholderi	ношо ва	Q5gh56 rattus norv	_	Q84zwl pisum sativ	Q4nqh4 anaeromyxob	_	Q5gh49 fugu rubrip					Q5zpa2 angiococcus	Q5gh65 mus musculu	Q5gh40 brachydanio	-	Q5gh57 rattus norv		Q8kby2 chlorobium	Q5cpz7 cryptospori	_	_		_		_	•	Q99aq7 torque teno	Q4nxl6 anaeromyxob
	1D	O25271 LEPDE	Q9F7V7_RHILV	Q4LK44 9BURK	QSGH72 HUMAN	Q5GH56_RAT	Q5GH64 MOUSE		Q4NQH4 9DELT	QBR587 MOUSE	Q5GH49_FUGRU		P97035 HAESO	Q5U414 XENLA	Q52DS6 ORYSA	Q5ZPA2 9DELT	Q5GH65 MOUSE	O5GH40 BRARE	O52E69 MAGGR	XKR6 RAT	XKR6 HUMAN	SYL CHLTE	QSCPZ7 CRYPV	Q9RYR0 DEIRA		Q7VV93 BORPE	Q7W7P3 BORPA	Q7WL31_BORBR	Q8KBA7 CHLTE	Q98D97_RHILO	Q99AQ7_9VIRU	O4NXL6_9DELT
	DB	~	~	7	7	~	~	~	~	~	~	~	~	7	N	~	N	~	~	-	н	-	~	~	N	~	~	~	7	~	~	7
	Query Match Length	670	735	408	579	580	580	488	188	298	578	627	240	486	910	385	540	580	618	638	641	807	2484	178	219	278	278	278	376	386	426	433
*	Query	55.1	53.1	52.0	51.0	51.0	51.0	50.0	49.0	49.0	49.0	49.0	48.5	•	48.0	46.9	46.9	46.9	46.9	46.9	46.9	46.9	46.9	45.9	45.9	45.9	45.9	45.9		45.9	45.9	45.9
	Score	54	52	51	20	20	20	49	48	48	48	48	47.5	47	47	46	46	46	46	46	46	46	46	45	45	45	45	45	45	45	45	45
	Result No.	1	7	e	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19		21	22	23	24	52	26	27	28	29	30	31

Q8xg08 ralstonia s Q5vrm7 oryza sativ	Oscilla staphylococ Qshnfl staphylococ Qshnfl staphylococ	. Q88uq8 Iaccobaciii Q5jh98 pyrococcus Q9cyy6 mus musculu	Q8bi07 mus musculu Q8k015 mus musculu Q8x076 neurospora	Q86wv6 homo sapien Q7nkw3 gloeobacter Q82tz1 nitrosomona
Q8XG08_RALSO Q5VRM7_ORYSA	OSXGZZ XENLA SYL STAEP SYL STAEQ	Q88UQ8_LACPL Q5JH98_PYRKO Q9CYY6_MOUSE	QBRIO7_MOUSE QBK015_MOUSE QBX076_NEUCR	Q86WV6_HUMAN Q7NKW3_GLOVI Q82TZ1_NITEU
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24.5	45 45 45	4 4 5 2 4 5	4 4 4 0 0 4	444
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32	3 9 4 3 6 4 6	33 38 38	4 4 4 0 L 2	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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                                                                                                                                                                                                                                             Leptinotarsa decemlineata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.1%; Score 54; DB 2; Length 670; 43.8%; Pred. No. 7.5; tive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1
SEQUENCE 670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00826; Hemocyanin.
InterPro; IPR05203; hemocyanin.
InterPro; IPR05204; hemocyanin.
Pfam; PF03723; Hemocyanin.
Pfam; PF03723; Hemocyanin.
Pfam; PF03722; Hemocyanin.
Pfam; PR03722; Hemocyanin.
PR051725; PR00187; HAEMOCYANIN.
PR051725; PR00187; HAEMOCYANIN.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Diapause protein 1 (Fragment).
670 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      potâto beetle.";
J. Insect Physiol. 40:527-535(1994).
EMBL; X76680; CAA53691.1; -; mRNA.
HSSP; P04253; ILLI.
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PRT;
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RKFYGALWSYLRHFFG 366
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Q9F7V7;
Q25271 LEPDE PRELIMINARY;
Q25271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Leptinotarsa.
NCBI_TaxID=7539;
[1]
NUCLEOTIDE SEQUENCE.
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09F7V7 RHILV

ID 09F7V7 R

AC 09F7V7;

DT 01-MAR-2(

DT 01-MAR-2C

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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q5GH72 HUMAN
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RO; GO:0016021; C:integral to membrane; IEA.

RO; GO:0016021; F:ATP binding; IEA.

RO; GO:0016021; F:ATP asea activity; IEA.

RO; GO:000166; F:ATPase activity; Coupled to transmembrane m. .; IEA.

RO; GO:000166; F:mucleotide binding; IEA.

RO; GO:000166; F:mucleotide binding; IEA.

RO; GO:000166; F:protein transport; IEA.

RO; GO:0006565; F:protein transport; IEA.

RO; GO:0006569; F:protein transport; IEA.

RO; GO:0006669; P:protein transport; IEA.

RO; GO:0006669; P:protein transport; IEA.

RO; GO:0006669; P:protein transport; IEA.

RITEPPO; IRR011327; ADA membrane 1.

RITEPPO; IRR011327; ADA membrane 1.

RITEPPO; IRR011327; ADE membrane 1.

RITEPPO; IRR01132; Type I sec_HlyB.

ROM; RO; ROS; ABC_tran; I.

RODOM; PRO00006; ABC_transporter; 1.

RODOM; PRO00011; ABC_TRANSPORTER; 1.

ROSITE; PSS0929; ABC_TRANSPORTER; 1; 1.

RROSITE; PSS0921; ABC_TRANSPORTER; 2; 1.

RROSITE; PSS0920; PEPTIDASE_C39; I.

RROSITE; PSS0920; PEPTIDASE_C39; I.

RROSITE; PSS0920; PEPTIDASE_C39; I.

RROSITE; PSS0920; PEPTIDASE_C39; I.
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Copeland A., Lucas S., Lappidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pilluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                     MEDLINE=21160352; PubMed=11467725; DOI=10.1139/Cjm-47-6-495; Venter A.P., Twelker S., Oresnik I.J., Hynes M.F., Manalysis of the genetic region encoding a novel rhizobiocin from Rhizobium leguminosarum bv. viciae strain 305."; Can. J. Microbiol. 47:495-502(2001).
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Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                               Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.1%; Score 52; DB 2; Length 735; 62.5%; Pred. No. 17; 4; Indels ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AF273216; AAG25076.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created) 13-SEP-2005 (TrEMBLrel. 31, Last seq 13-SEP-2005 (TrEMBLrel. 31, Last ann Hypothetical protein. ORFNames=Bcen2424DRAFT_1071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkholderia cenocepacīa HI2424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4LK44 9BURK PRELIMINARY;
Q4LK44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                  NCBI_TaxID=387;
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041.K44 9B
11D 041.K44 9B
11D 041.K4 9B
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvēgicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
STRAIN=H12424;
US DOD Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                  -1- CAUTION: The sequence shown here is derived from an BMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAHLO1000063; EAM16412.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                            52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 13; ive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang C.-H., Chen Y.; "A superfamily of XK-related genes (XRG) widely expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS34245; AAT07094.1; -; mRNA.
SEQUENCE 579 AA; 63825 WW; DBDOFF64B9EDD53D CRC64;
                                                                                                     HI2424.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
XK-related protein 7.
Homo sapiens (Human).
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Last annotation update)
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58.3%; Pred. No. 28;
ive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSGH72_HUMAN PRELIMINARY;
QSGH72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :||::|| |
190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 47.1 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RAT
Q5GH56_RAT PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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RESULT 9
QBR587 MOUSE
ID QBR587 MC
AC QBR587;
DT 01-JUN-20
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Matches
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Matches
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Q4NQH4 9D
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                       Gaps
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"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX53423; ATT07102.1; ; mRNA.
MGI; MGI:3556711; AX534253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 2; Length 580;
Pred. No. 28;
3; Mismatches 2; Indels
                                                                                                                       2; Length 580
vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY534261; AAT07110.1; -; mRNA.
SEQUENCE 580 AA; 64337 MW; 8F4907F391B4F5BE CRC64;
                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA; 64301 MW; F3291FABF4C5A826 CRC64;
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-1- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AF537321; AAO23063.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             580 AA
                                                                                                                     Score 50; DB 2; Pred. No. 28; 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 51.0%;
Local Similarity 58.3%;
hee 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                          51.0%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, KK-related protein 7. Name-AY534253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pisum sativum (Garden pea).
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QSGH64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || :||::|| |
190 LGQVWRYLRALY 201
                                                                                                      Ouery Match
Best Local Similarity 58.3.
Best Local 7; Conservative
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Q842W1 PEA PRELIMINARY;
Q842W1;
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190 LGQVWRYLRALY 201
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                                                                                                                                                                                                                         6 LGSIWRFIRAFY 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
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084 ZM1 PE
10 084 ZM1
084 ZM1
01-40
DT 
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GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
InterPro; IPR00129; Cytochrome_P450.
InterPro; IRR002401; EP4501.
Pfam; PF00067; p450; 1.
PRINTS; PR00485; BE4501.
PRINTS; PR00485; PE50.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 188;
                                                                                                                                                                                                                                                                                                                                                Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AAHD01000035, EAL77797.1; -; Genomic_DNA.
SEQUENCE 188 Aa; 21278 MW; 6DEAFDBF874C4721 CRC64;
                                                                                                                                                                                                                                                                                        488 AA; 56478 MW; 503453CB6E43C830 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBR587_MOUSE PRELIMINARY; PRT; 298 AA. 0,8R587; 01-UN-2002 (TrEMBLrel. 21, Created) 01-UN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSI------WRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 49.0%; Score 48; DB 2; 1 Similarity 30.6%; Pred. No. 18; 11; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                          50.0%; Score 49; DB 58.3%; Pred. No. 34; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4NQH4_9DELT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 FLGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|::| |:|||
54 FIGNMWSFLRAF 65
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ORFNames=AdehDRAFT 0950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
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Gaps

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3; Indels

627 AA.

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MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Histophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97221585; PubMed=9068631;
Pontarollo R.A., Rioux C.R., Potter A.A.;
"Cloning and characterization of bacteriophage-like DNA from Haemophilus somuns homologous to phages P2 and HP1.";
J. Bacteriol. 179:1872-1879(1997).
vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS34268; AAT01117.1; -; mRNA.
SEQUENCE 578 AA; 66214 MW; 8915B2A30D38E80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 AA; 69724 MW; BBE187A53BF96229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain, PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
01f13; not preceded by a good RBS site (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                  Score 48; DB 2;
Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BA000022; BAA18591.1; -; Genomic_DNA.
PIR; S76462; S76462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                    58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-JUN-2003 (TrEMBLrel. 24, S111858 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=s111858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESCUE, P97035 HAESO PRELIMINARY; TO P97035 HAESO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      P74489 SYNY3 PRELIMINARY;
                                                                                                                                                                                                                                                185 LGQVWRYIRTMY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                             Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                  6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 3:109-136(1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               P74489
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                                                                                                                                                                                                                                                   TISSUE=Mammary tumor metastatized to lung. MMTV-ITR/Wnt1 model.

Expression driven by an MMTV-ITR enhancer.;

Expression driven by an MMTV-ITR enhancer.;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Nillalon D.K., Muxny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rabes J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

R Hench M., Reminital analysis of more than 15,000 full-length human and mouse CDNA seminances "."
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                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Verčebrata; Euteleostomi, catinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthopterygii, Percomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes; Tetradontoidea, Tetraodontidae, Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.0%; Score 48; DB 2; Length 298; 41.2%; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
XK.related protein 6.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2002) to the BMBL/GenBank/DDBJ databases. EMBL; BC023148; AAH23148.1; -; mRNA. Ensembl; ENSMUSG0000020652; Mus musculus. MGI; MGI:1923800; 2810429005Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA; 34043 MW; 664CE91435D9DDF8 CRC64;
    01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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171 VQRFLFSLWAYLNAYAG 187
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OSGH49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
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                           2810429005Rik protein.
Name=2810429005Rik;
                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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nes 7; Conserv
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                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                STRAIN=CZECH II;
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RESULT 10 Q5GH49_FUG

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DB 2; Length 627; 64;

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TISSUE-Kidney.

WEDINE-EXIGNEY.

ALGEBLINE-EXIGNEY.

ALGEBLINE-EXIGNEY.

Rausher R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Algebria R.L., Feingold B.A., Wagner L., Shenmen C.M., Schuler G.D.,

Algebria R.E., Collins F.S., Wagner L., Shanefer C.F., Bhar N.K.,

Algebria R.F., Jordan H., Moore T., Max S.I., Wang J., Halth F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raba S.S., Morley K.C., Hale S., Garranci P., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garranci P., Glubbs R.A.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Glubbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A. Green E.D., Dickson M.C.,

Ratchiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rederment D. M., Madan A., Young S.J.M., Marra M.A.;

Redermention and initial analysis of more than 15,000 full-length human
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                                                                                                                                     Gaps
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-!- SUBCELLIAR LOCATION: Integral membrane protein (By similarity).
EMBL, BCO85081, AAH85081.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xeyopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                     1;
                                                                                                          DB 2; Length 240;
                                                                                                                                     5; Indels
                           Pontarollo R.A.;
Thesia (1996), V. I. D. O., University of Saskatchewan.
EMBL; U28154; AAC45167.1; -; Genomic_DNA.
NON_TER 240 240
                                                                     240 240 240 MW; 63348D8619BBAC30 CRC64;
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                                                                                                                                                                                                                                                                                      01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
LOC495492 protein (Fragment).
                                                                                                        48.5%; Score 47.5; I
57.9%; Pred. No. 28;
:ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                               QSU414_XENLA PRELIMINARY;
                                                                                                                          Best_Local Similarity 57.9
Matches 11; Conservative
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  NUCLEOTIDE SEQUENCE.
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                 STRAIN=HS25
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SEQUENCE
                                                                                                             Query Match
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MEDLINE=2333736; PubMed=12447438; DOI=10.1038/nature01184;
RA Saaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Saaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Kanamori H.,
RA Mu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Msukawa M., Arikawa K., Chiden Y., Hayashi M.,
Adamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RATA Ikeno M., Ito S., Ito T., Ito Y., Ito Y., Inabuchi A., Kamiya K.,
Arasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishim M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Shibata M.,
Naki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Naki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Anto M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
Naki K., Mangata H., Rado T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
The genome sequence and structure of rice chromosome 1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Rokaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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73
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EMBL; AP002868; BAD52586.1; -; Genomic_DNA.
R GO; GO:0005355; F:glucose transporter activity; IEA.
R GO; GO:0005351; F:sugar porter activity; IEA.
R GO; GO:0005251; F:ransporter activity; IEA.
GO; GO:0008643; F:ransporter activity; IEA.
R InterPro; IPR000803; Gluc_transporter.
R InterPro; IPR001863; Sugar_transporter.
R InterPro; IPR005828; Sub transporter.
R InterPro; IPR005829; Sug_transporter.
R InterPro; IPR005829; Sug_transporter.
R PRINTS; PR00172; GLUCTRNSPORT.
R PRINTS; PR00172; GLUCTRNSPORT.
R PRINTS; PR00171; GUGAR TRANSPORT.
R TIGRPAM; TIGRO0879; SSP; 1.
R PROSITE; PS08609; MFS; 1.
R PROSITE; PS08609; MFS; 1.
R PROSITE; PS08601; RIGAR_TRANSPORT 2; UNKXOWN_1.
Sugar_transport; Transmembrane; Transport.
J NON TER
SEQUENCE 486 AA; 54035 MW; E333F97CD90A1119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 486;
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GO; GO: 0004823; F:Leucine-tRNA ligase activity; IEA.
GO; GO: 0006423; F:Leucine-tRNA aminoacylation; IEA.
GO; GO: 0006429; F:Leucine-tRNA aminoacylation; IEA.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001300; tRNA-synt_I.
Pfam; PP001313; tRNA-synt_I.
PRINTS; PR00995; TRNASYNTHLEU.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative leucyl-tRNA synthetase.
Name=P0698A04.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%; Score 47; DB 2; 50.0%; Pred. No. 70;
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QSZDS6;
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Best Local Similarity 50.0
Matches 9; Conservative
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Biosynthesegenclusters aus dem Myxobakterium Angiococcus disciformis
An 488.",
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ620477; CAF05655.1; -; Genomic_DNA.
InterPro; IPR001064; Crystallin.
InterPro; IPR001064; Crystallin.
PROSITE; PS50915; CRYSTALLIN BETAGAMMA; 2.
PROSITE; PS50915; ZINC_PROTEĀRĒ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                         Gaps
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TIGREAMS; TIGRO0396; leus bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE 1; 1.
ATP-binding; Aminoscyl-tRNA synthetase; Ligase; Nucleotide-binding;
Protein biosynthesis.
SEQUENCE 910 AA; 102551 MW; ES856521EC817196 CRC64;
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OSZPAZ;
OSZPAZ;
OSZPAZ;
DS-OCT-2004 (TrEMBLrel: 28, Last sequence update)
25-OCT-2004 (TrEMBLrel: 28, Last sequence update)
25-OCT-2004 (TrEMBLrel: 28, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Angiococcus disciformis.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Cystobacterineae; Cystobacteriaes
                                                                                                                                                                                                                                      Query Match

48.0%; Score 47; DB 2; Length 910;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels
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46.9%; Score 46; DB 2; Length 385;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 4; Mismatches 4; Indels
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10 052PA3
AC 052PAA
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Search completed: March 29, 2006, 01:49:11 Job time : 168.938 secs

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Sequence 242, Application US/08940095

Sequence 242, Application US/08940095

Sequence 242, Application US/08940095

Sequence 242, Application US/08940095

Section US/080405

Settle No. 6004925

Sequence Application

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Man Their USF TO TREAT DYSLIPIDEMIC DISORDERS

TITLE OF INVENTION: AND THEIR USF TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

COTTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGRAT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 10 NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: NO. 6004925e
US-08-940-095-242
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TYPE: amino acid
STRANDEDNESS: single
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COUNTRY:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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39.487 Million cell updates/sec
                                                                                                          March 29, 2006, 01:49:32; Search time 37.6875 Seconds
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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.: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

.: /cgn2_6/ptodata/1./iaa/6_COMB.pep:*

.: /cgn2_6/ptodata/1./iaa/H_COMB.pep:*

.: /cgn2_6/ptodata/1./iaa/PGTUS_COMB.pep:*

.: /cgn2_6/ptodata/1./iaa/RE_COMB.pep:*

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US-09-328-352-8162
US-08-132-767-50
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US-09-465-718-242
US-09-205-258-892
US-10-004-860-892
US-10-799-870-49
US-10-799-870-45
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US-09-453-841-242

US-09-453-832-242

US-09-453-826-242

US-09-453-840-242

US-09-865-989-242

US-09-453-834-242
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-09-710-279-340
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Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Score Match Length DB
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US-09-902-540-15932
US-09-538-092-643
US-08-480-190-3
US-08-480-190-3
US-08-477-259A-3
US-08-480-190-2
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US-08-488-379-1
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                                             Gaps
                                                                                                                                                                                                                                                                                APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CORTY: New York
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Pred. No. 1e-05;
4; Mismatches 1; Indels
Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           009196-0006-999
                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                            Sequence 242, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 242, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LGURTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00915
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERAX: 66141 PENNIE
TELEX: 66141 PENNIE
TENTEN: 18 amino acide
TYPE: amino acide
                                                                                                         1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
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                                                                                    1 GIRRFLGSIWRFIRAFYG 18
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; MOLECULE TYPE: No. 6037323e

US-08-940-093-242
  79.6%;
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                               US-08-940-093-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NO COUNTRY:
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Gaps
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Fatent No. 6265377
Fatent No. 6265370
FAPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I ACONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OP SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                          STATE: NY
STATE: NY
COUNTRY: USA
ZIP: 1006-281
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VErsion 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER: 00/096
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEBHONE: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78; DB 2;
Pred. No. 1e-05;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: No. 6046166e

US-08-940-096-242
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2811
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Gaps ö

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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexl, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITT: New York
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
REFERENCE/DOCKET NUMBER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 2;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING STSTEM: DOS
SOFTWARE: FREEERO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFFCATION:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 650-493-5556
TELEFAK: 650-493-5556
TELEFAK: 650-493-5556
TELEFAK: 65141 PENNIE
INFORMATION FOR SECIED NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 242, Application US/09453838 Patent No. 6376464 GENERAL INFORMATION:
                          TELECOMMUNICATION INFORMATION TELEPHONE: 650-493-4935
                                                    TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                      INFORMATION FOR SEQ ID NO: 242: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acid TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GIRRFLGSIWRFIRAFYG 18
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E: No. 6376464e
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: No. 6376
US-09-453-838-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Com
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Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
Sekul, Renate
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                 APPLICATION NOMBER: US/09/403,/13
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COUNZI, LAURA A REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEFONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-6556
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-No. 6323341-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: «Unknown-
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,742
  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESE Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: No. 6265377e
US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-453-605-242
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MOLECULE TYPE: No. 6573239e
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 amino acids
                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
Patent No. 6573239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-453-841-242
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US-09-453-833-242
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                                                                                                                                                                                                                                                                                                             APPLICANT: Sekul, Klaus
APPLICANT: Sekul, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-1 AGONISTS AND THEIR
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESSED ADRESS:
ADDRESSED: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NI

COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDLUM TYPE: Diskettee
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
TILING DATE:
APPLICATION NUMBER:
TILING DATE:
ATTORNEY/AGBNT INFORMATION:
NAME: COLUZZI, LAUIR A
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELEPONIUNICATION INFORMATION:
TELEPONIUNICATION INFORMATION:
TELEPONIUNICATION INFORMATION:
TELEPONIUNICATION OF SEG ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
FIRE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78; DB 2;
Pred. No. 1e-05;
                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                 Sequence 242, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
                                                                                                1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                       1 GIRRFLGSIWRFIRAFYG 18
                    79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: NO. 6518412e
US-08-940-136-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                    Best Local Similarity 72.2
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                   US-08-940-136-242
                    Query Match
                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         윱
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APPLICANT SEALS MEASUREM, Cash Louis
APPLICANT SEALS MEASUREM, Cash Louis
APPLICANT SEALS MEASUREM, Cash Louis
APPLICANT SEALS MEASUREM CONTUCT ISABELS
APPLICANT: COTTUCT ISABELS
APPLICANT: COTTUCT ISABELS
TITLE OF INVESTION: APOLITICAN METALS
TITLE OF INVESTION: APOLITICAN METALS
ADDRESSER: Pethis & Edward Lip
ADDRESSER: Pethis & Edward L
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US-09-453-840-242

US-09-453-840-242

Sequence 242, Application US/09453840

Sequence 242, Application US/09453840

Sequence 242, Application US/09453840

Sequence 242, Application US/09453840

Sequence 242, Application

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Sekul, Renate

APPLICANT: Met., Gunther

APPLICANT: Met., Gunther

APPLICANT: Met., Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

CTAT: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    009196-0004-999
                                                                                                                        009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FaatSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFTLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 09196-(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/940,095
                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00919
TELECOMMUNICATION INFORMATION:
TELERHONE: 650-493-4935
TELERA: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||::||||||:||:|| || GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: anino acid
TYPE: alingle
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: CONTRY TO THE TOTAL TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-453-826-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Baseux, Jean-Louis
APPLICANT: Battner, Klaus
APPLICANT: Bekut, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLITOR OF A PREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCES: 258
CORRESPONDENCE S.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
CONDUTER: BATABABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION DATA:
CURRENT APPLICATION NUMBER: US/09/453,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
                                                                                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUYA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0
TELECHONICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 242:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242, Application US/09453826
Patent No. 6630450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 6602854e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                           ZIP: 10036-2811
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
            New York
                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-453-826-242
                                                              COUNTRY:
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                   Gaps
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                                                                                            Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSGQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

CLASSIFICATION: «Unknown»

PRIORNEY/AGRIT ON UNMBER: 09/465,719

FILING DATE: 17-DEC-1999

ATTORNEY/AGRIT INFORMATION:

NAME: COTUZZI, LAUTA A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0006-999

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 6734169e SEQUENCE DESCRIPTION: SEQ ID NO: 242: US-09-865-989-242
                                                                                                                                                                                                                                                                                                  Sequence 242, Application US/09865989 Patent No. 6734169 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                   ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                            79.6%;
                                                                             Query Match
Best Local Similarity 72.27
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.4
Best Local 3; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                                     RESULT 12
US-09-865-989-242
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US-09-453-834-242

| Sequence 242, Application US/09453834
| Sequence 242, Application US/09453834
| Patent No. 6753313
| GENERAL INFORMATION:
| APPLICANT: Backl, Renate
| APPLICANT: Sekul, Renate
| APPLICANT: Butner, Klaus
| APPLICANT: Butner, Klaus
| APPLICANT: Cornut, Isabelle
| APPLICANT: Metz, Gunther
| APPLICANT: Dufourcq, Jean
| TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
| UNMBER OF SEQUENCES: 258
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 242, Application US/10283599
Patent No. 6844327
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COCALZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,0196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFRX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWEENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: No. 6753313e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Ave
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-283-599-242
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Query Match

79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
FILING DAIE:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
ATCREY/AGENT INFORMATION:
NAME: COLUZZI, Laura A
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
FILECHMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEPHONE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
"""DEF: amino acids
"""DEF: amino acids
"""DEF: amino acids
"""DEF: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: March 29, 2006, 01:51:15 Job time : 38.6875 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6900177e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-465-718-242
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US-09-465-718-242

US-09-465-718-242

Squence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Basseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Gent, Renate

APPLICANT: Gornut, Isabelle

APPLICANT: Gornut, Isabelle

APPLICANT: Gornut, Isabelle

APPLICANT: Metz, Gunther

ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STATE: NY

COUNTRY: USA

INSA

ZIP: 10036-2811

COMPUTER: ISM Compatible

COMPUTER: ISM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   009196-0007-999
                                                                                               CITY: New York
STATE: NY
COUNTY: USA
ZIP: 10036-2811
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELTE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Veration 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CCT-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/40,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTULEA', LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEFRA: 66141 PERNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                    SSEE: Pennie & Edmonds LLP
T: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
       NUMBER OF SEQUENCES: 274
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserva
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Sequence Seq

Sequence Sequence Sequence

Perfect score:

Sequence:

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Scoring table:

Searched:

Minimum DB Maximum DB

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US-10-712-447-2

| Sequence 2, Application US/10712447
| Sequence 2, Application US/10712447
| Sequence 2, Application No. 1020040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANNATHARMIAH, GATTADAHALLI M. |
| APPLICANT: GARBER, DAVID W. |
| APPLICANT: GARBER, DAVID W. |
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE |
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE |
| TITLE OF INVENTION NUMBER: 105/10/712,447 |
| CURRENT FILING DATE: 2003-11-13 |
| PRIOR APPLICATION NUMBER: 60/425,821 |
| PRIOR FILING DATE: 2002-11-13 |
| NUMBER OF SEQ ID NOS: 210 |
| SOFTWARE: Patentin Ver. 3.2
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Sequence 5, Application US/10712447

Sequence 5, Application US/10712447

PUBLICATION NO. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILLE REPERENCE: 112739-12308

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
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                     US-10-712-447-15

US-10-712-447-19

US-10-712-447-19

US-10-712-447-56

US-10-712-447-56

US-10-712-447-79

US-10-712-447-94

US-10-712-447-94

US-10-712-447-91

US-10-712-447-41

US-10-989-242

US-10-99-574A-242
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; OTHER INFORMATION: c-term amidated
US-10-712-447-2
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LENGTH: 18
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Matches 18
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116, App
129, App
131, App
131, App
53, App
74, Appl
4, Appl
127, App
19, Appl
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Sequence 5, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 13, Appl
Sequence 91, Appl
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Sequence 116, R
Sequence 117, R
Sequence 129, R
Sequence 131, R
                                                                                                               March 29, 2006, 02:05:02 ; Search time 153 Seconds (without alignments) 49.156 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-13
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US-10-712-447-14
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US-10-712-447-118
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US-10-712-447-119
US-10-712-447-119
US-10-712-447-114
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US-10-712-447-121
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                                                                                                                                                                                                                                                                                              1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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98
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SOFTWARE: Patentin Ver. 3.2
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                        SEQ ID NO 10
LENGTH: 18
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APPLICANT: ANANTHARAMAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 05/425,821
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 8
LENGTH: 18
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WS-10-712-447-10

Sequence 10, Application US/10712447

Publication No. US20640186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF PRESENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION UNBER: 60/425,821

NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide US-10-712-447-8
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100.0%; Pred. No. 8.8e-08;
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PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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Publication No. US20040186057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
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US-10-712-447-8
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US-10-712-447-13

Sequence 13, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SOUTHOUSE: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATCHING DATE: 2002-11-13

LEMOTH: 18

LEMOTH: 18

TYPE: PRT
ORGANISM: Artificial Sequence
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Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHEITC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHEITC SINGLE DOMAIN POLYPEPTIDES
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT PILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
SOFTWARE: PALENTIN VET: 3.2
SOFTWARE: PALENTIN VET: 3.2
LENGTH: 18
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                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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Pred. No. 8.8e-08;
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100.0%; Pred. No. 8.8e-08;
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                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 18; Conservative
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Sequence 116, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GESTA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLIFOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-1239

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER: OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                  Sequence 115, Application US/10712447

Sequence 115, Application US/10712447

Publication No. US20040186057A1

GENERAL INPORMATION:
APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLICEDROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-1210S

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN VET. 3.2

LENGTH: 18
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                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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Pred. No. 3.5e-07;
2; Mismatches 0; Indels
                                                                                                                                 Query Match

96.9%; Score 95; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 1; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative ;
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| Sequence 117, Application No. US20040186057A1
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANATHARANIAH, GATTADAHALLI M.
| APPLICANT: DATTA, GEETA
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APPLICANT NOWBER: US/10/712,447
| CURRENT APPLICATION NUMBER: US/10/712,447
| CURRENT APPLICATION NUMBER: US/10/712,447
| CURRENT APPLICATION NUMBER: 06/425,821
| PRIOR FILING DATE: 2002-11-13
| NUMBER OF SEQ ID NOS: 210
| SEQ ID NO 117
| LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 129, Application US/10712447

Sequence 129, Application US/10712447

Sequence 129, Application US/10712447

Sequence 120, US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANNITHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR PAPLICATION NUMBER: 60/425,821

SHOR RAPLICATION NUMBER: 60/425,821

SHOR RAPLICATION NUMBER: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

SEQ ID NOS: 210
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic;
CTHER INFORMATION: peptide
US-10-712-447-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ', OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: peptide US-10-712-447-117
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-10-712-447-116
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Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels
                                                                                                    Length 18,
                                                                                                      Score 94; DB 4; I Pred. No. 3.5e-07;
                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                         95.9%;
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Best Local Similarity 88.99
Matches 16; Conservative
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Gaps

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Indels

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Mismatches
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Publication No. US20040186057A1
GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 53, Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
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                                              1 GIRRFLGSIWRFIRAFYG 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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NAME/KEY: MOD RES
LOCATION: (14)
OTHER INFORMATION: (Dime) Ly8
US-10-712-447-53
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 74
  16; Conservative
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    Matches
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FUGURECE 21, Application US/10712447

FUGURECE 21, Application No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GETA

TITLE OF INVENTION: APPLICANT ENVERTICE SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANT ENVERTICE SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANT SINGLE DOMAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

LENGTH: 18
                                                                                                                                                                                                                                             Sequence 131, Application US/10712447

Publication No. US20040186057A1

Sequence 131, Application US/10712447

Publication No. US20040186057A1

APPLICANT: ANNATHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: MATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLICANOREN E ADOLIPORROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-12308

CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN Ver. 3.2

LENGTH: 18
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-10-712-447-21
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Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94; DB 4; Length 18;
Pred. No. 3.5e-07;
2; Mismatches 0; Indels
                         Score 94; DB 4; Length 18;
Pred. No. 3.5e-07;
                    ch
1 Similarity 88.9%; Pred. No. 3.5e
16; Conservative 2; Mismatches
                                                                                                                   1 GIRRFLGSIWRFIRAFYG 18
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88.9%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
                         Query Match
Best Local Similarity
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Best Local Similarity
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                                                                       Matches
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APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ARABER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SPOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 60/425,821
PRIOR PELLING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VET: 3.2
SEQ ID NO 53
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANATHARAMIAH, GATTADAHALLI M.
APPLICANT: ARBER, DAVID W.
APPLICANT: CARBER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLICANTON: APPLICANTON NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 00/425,821
PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide PEATURE: NAME/KEY: MOD_RES LOCATION: (3)
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Pred. No. 7.1e-07;
2, Mismatches 0, Indels
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US-10-712-447-4

i Sequence 4, Application US/10712447

j Sequence 4, Application US/10712447

j Publication No. US20040186057A1

j GENERAL INFORMATION:

j APPLICANT: ANAWITHARANIAH, GATTADAHALLI M.

j APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

LENGTH: 18
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Best Local Similarity 94.4%; Pred. No. 1.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                          Query Match
93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
PEATURE:
; OTHER INFORMATION: peptide US-10-712-447-74
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Search completed: March 29, 2006, 02:10:39 Job time : 153 secs

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March 29, 2006, 02:06:17; Search time 16.875 Seconds (without alignments) 31.461 Million cell updates/sec
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1. /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*
2. /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*
3. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*
4. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*
5. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*
6. /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7. /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*
8. /SIDSS/ptodata/1/pubpaa/US11_NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      174695 segs, 29494374 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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98
1 GIRRFLGSIWRFIRAFYG 18
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

;	A.	4	Α,	App	App	App	Αp	App	Appl	App	Ap	Αp	Αb	Αb	Ap		Αp								
	16673	16672,	16671,		206,	229,	īŌ	198,	54, A	521,	1491,	1644,	1700,	2589,	2733,	3648,	4073,	4652,	4677,	4777,	4910,	6009	6227,	6781,	6911,
Description		Seguence	Sequence		Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence			Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence
ΩI	US-11-096-568A-16673	US-11-096-568A-16672	US-11-096-568A-16671	US-10-793-626-340	US-09-978-360A-506	US-11-172-740-229	US-10-821-234-1575	US-10-485-517-198	US-10-392-234A-54	US-11-087-099-521	US-11-087-099-1491	US-11-087-099-1644	US-11-087-099-1700	US-11-087-099-2589	US-11-087-099-2733	US-11-087-099-3648	US-11-087-099-4073	US-11-087-099-4652	US-11-087-099-4677	US-11-087-099-4777	US-11-087-099-4910	US-11-087-099-6008	US-11-087-099-6227	US-11-087-099-6781	US-11-087-099-6911
DB	7	2	2	9	Ŋ	7	9	9	9	7	7	7	7	7	~	7	7	۲	7	7	7	7	7	7	7
% Query Match Length	306	327	360	539	379	85	365	805	265	394	394	394	394	394	394	394	394	394	394	394	394	394	394	394	394
* Query Match	45.9	45.9	45.9	45.9	44.9	42.9	42.9	42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
Score	45	45	45	4.5	44	42	42	4.2	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
Result No.	-	2	(1)	4	'n	4	7	· 00	ď	10	11	12	13	14	15	16	17	18	10	20	21	22	23	24	25

AP AP	A A A A A	A A A	4444	AAAQA
7139, 7287, 7806,	926, 8706, 8837, 9004,	9973, 10104, 10325,	10517, 11001, 11036,	11905, 12199, 12453, 6018, 26625,
	Sequence 8 Sequence 8 Sequence 8		Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence
US-11-087-099-7139 US-11-087-099-7287 US-11-087-099-7806	US-11-087-099-7928 US-11-087-099-8706 US-11-087-099-837 US-11-087-099-9004	US-11-08-09-973 US-11-087-099-9973 US-11-087-099-10104 US-11-087-099-10325	US-11-087-099-10517 US-11-087-099-11001 US-11-087-099-11036 US-11-087-099-11514	US-11-087-099-11905 US-11-087-099-12199 US-11-087-099-12453 US-11-087-099-6018 US-11-096-568A-26625
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41.8 41.8 8.1.8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 1 . 8 1 . 8 8 . 1 1 . 8 . 8	41.8 41.8 41.8	41.8 41.8 41.8 41.8
4 4 4 1 1 1 1	4444	4 4 4 4	4444	44444
26 27 28	22 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		338 388 40 40	4 4 4 4 4 1 4 5 4 5

# ALIGNMENTS

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Sequence 16672, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICAT: Alexandrov, Nickolai et al.
| APPLICAT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby:
| TITLE OF INVENTION: Therby:
| TITLE OF INVENTION: Therby:
| TITLE OF INVENTION: US/11/096,568A
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 16672
US-11-096-568A-16673
US-11-096-568A-16673
US-2010-007-11-096-568A-16673
Publication No. US20060048240A1
Publication No. US20060048240A1
GENERAL INFORMATION: Squence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 16673
TENGTH: 306
TYPE: PRT
CURRENT: APPLICATION NUMBER: US/11/096,568A
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Pred. No. 5.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)._(306)

OTHER INFORMATION: Ceres Seq. ID no. 12353656
US-11-096-568A-16673
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Best Local Similarity 58.3%;
Matches 7; Conservative 3
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US-11-096-568A-16672
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4 RFLGSIWRFIRAFYG 18
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357 GSRRFLDRVWRLI 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-978-360A-506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL LOCATION: -37...-
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 16671
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIWMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 340
LENGTH: 539
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                                                                                                                 Score 45; DB 7; Length 327; Pred. No. 6; 2; Indels 3; Mismatches 2; Indels
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45.9%; Score 45; DB 6; Length 539;
Best Local Similarity 61.5%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 7; Length 360;
Pred. No. 6.5;
3; Mismatches 2; Indels
                        the COCATION: (1)...(327)
COTHER INFORMATION: Ceres Seq. ID no. 12353655
US-11-096-568A-16672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // NAME/KEY: misc_feature
// LOCATION: (1)..(360)
// OTHER INFORMATION: Ceres Seq. ID no. 12353654
US-11-096-568A-16671
                                                                                                                                                                                                                                                                                                                                                                        Sequence 16671, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%;
58.3%;
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ORGANISM: Artificial Sequence
                                                                                                                 Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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221 VRESLGSLWRFM 232
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Best Local Similarity 58.3
Matches 7; Conservative
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254 VRESLGSLWRFM 265
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NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                     US-11-096-568A-16671
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1 GIRRFLGSIWRFI 13

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Sequence 229, Application US/11172740
Sequence 229, Application US/11172740
Publication No. US20060057724A1
Sequence 229
Publication No. US20060057724A1
SERBRAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: BROWER, VAAcheala
APPLICANT: BROWER, VAAcheala
APPLICANT: BROWER, VAAcheala
APPLICANT: BROWER, VAAcheala
APPLICANT: BROWER 2750-1602PUSS
CURRENT APPLICATION NUMBER: US/11/172,740
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,621
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URABULTS.

URABULTS.

Sequence 506, Application US/0978360A

Publication No. US2006009633A9

GENERAL INFORMATION:

APPLICANT: Budwards Jean-Baptiste Dumas Milne

APPLICANT: Buclett, Aymeric

APPLICANT: Complementary DNA's Encoding Proteins with Signal Peptides

THIR PERERNET: 56. US4. (1P

THIR PERERNET: 56. US4. (1P

THIR PAPLICANTION: Complementary DNA's Encoding Proteins with Signal Peptides

THER PERERNET: 56. US4. (1P

THER PERERNET: 1997-11-13

PRIOR FILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-02-09

PRIOR PELICATION NUMBER: US 60/056, 116

PRIOR PELICATION NUMBER: US 60/056, 116

PRIOR PELICATION NUMBER: US 60/059, 123

PRIOR PELICATION NUMBER: US 60/059, 135

PRIOR PELICATION NUMB
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44.9%; Score 44; DB 5; Length 379;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 2; Mismatches 5; Indels
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Sequence 54, Application US/10392234A

Sequence 54, Application US/10392234A

Publication NO. US2005025538A1

Publication NO. US2005025538A1

APPLICANT: Pharmacia and Upjohn Corporation

APPLICANT: Buxeer, Steven

APPLICANT: Boole, Keith

APPLICANT: Decker, Douglas

APPLICANT: Notarni Li

APPLICANT: Notarni Li

APPLICANT: Siaznhi Li

PRIOR FILIR REFERENCE: 6206

CURRENT APPLICATION NUMBER: US/10/392,234A

PRIOR APPLICATION NUMBER: US 60/364,935

PRIOR FILING DATE: 2002-03-15

NUMBER OF SEQ ID NOS: 67

SEQ ID NO S.

LENGTH: 265
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                                                                                      Length 365;
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Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INVOKATION:
GENERAL INVOKATION:
GENERAL INVOKATION:
APPLICANT: Biosynexus Incorporated
APPLICANT: Boster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEC ID NO 198
LENGTH: 805
                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                          Sequence 198, Application US/10485517; Publication No. US20050256299A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.8%;
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42.9%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                        42.9%;
50.0%;
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623 GSRRFLDRVWRLM 635
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                                                                                                                                                                                                              :|| |||:| ::
127 VGSDWRFLRGYH 138
                                                                                      Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                              6 LGSIWRFIRAFY 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575
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Best Local Similarity
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                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (13)...(81)
OTHER INFORMATION: Pfam Name: PC4; Pfam Description: Transcriptional Coactivator p15
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: _ _ OTHER INFORMATION: Utility: Useful for making lethal plants for genetic confinement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Utility: Useful for making plants with increased biomass and foli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer; CTHER INFORMATION: inflorescences
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Sequence 1575, Application No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, I wan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
CURRENT FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOUTHARE: Pt SEQ_genes Version 1.0

SEQ ID NO 1575

LENGTH: 365
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OTHER INFORMATION: Utility: Useful for delaying flowering time
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                       PRIOR APPLICATION NUMBER: 60/584,829
PRIOR FLING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 229
LENGTH: 85
                                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IRRFLGSIWRFIRAFY 17
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                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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US-10-821-234-1575
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Best_Local Similarity 54.5%; Score 41; DB 7; Length 394; Matches 6; Conservative 3; Mismart.
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Publication No. US20060041961A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
TITLE OF INVENTION: Genes and Uses for Plant Improvement
TITLE OF INVENTION: Genes and Uses for Plant Improvement
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2589
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                           Sequence 1700, Application US/11087099
; Sequence 1700, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFRENCE 38-21 (53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT APPLICATION NUMBER: US/11/087,099
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2733, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Zea mays subsp. mays US-11-087-099-2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Zea mays subsp. mays US-11-087-099-1700
                                                           TYPE: PRT ORGANISM: Zea mays subsp. mays
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                                                                                                                                            41.8%;
NUMBER OF SEQ ID NOS: 12464
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Matches 6; Conservative
                                                                                                                                                                                  6, Conservative
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19 VGGMWAFLRAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LGSIWRFIRAF 16
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19 VGGMWAFLRAF 29
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19 VGGMWAFLRAF 29
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Best Local Similarity
Matches 6; Conserv
                                                                                                   US-11-087-099-1644
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US-11-087-099-2589
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                SEQ ID NO 1644
LENGTH: 394
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; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and USES for Plant Improvement;
FILE REFERENCE: 38-21 (53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1491
                                                                                                                                                                           Sequence 521, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILIE REPERENCE: 38-21(33450) B.P
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 521
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 7; Length 394; Pred. No. 31; Alsmatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Sequence 1644, Application US/11087099
PUDLication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
TILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 7;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(394); COTHER INFORMATION: unsure at all Xaa locations US-11-087-099-1491
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.8%;
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Best Local Similarity 54.5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.5
Matches 6; Conservative
5; Conservative
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19 VGGMWAFLRAF 29
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19 VGGMWAFLRAF 29
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US-11-087-099-521
  Matches
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Gaps

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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; SEQ ID NOS: 12464; SEQ ID NO 2733
LENGTH: 394; TYPE: PRT
TYPE: PRT
CRANISM: Zea mays subsp. mays
US-11-087-099-2733
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19 VGGWWAFLRAF 29
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Search completed: March 29, 2006, 02:11:16 Job time: 17.875 Bec8

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